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OM protein - protein search, using sw model

Run on: July 22, 2002, 17:12:45 ; Search time 30.04 Seconds

(without alignments)  
210,759 Million cell updates/sec

Title: US-09-581-894A-7  
Perfect score: 336  
Sequence: 1 LODRERSRRRCVRLHESCL.....FNATCYCRKLGTMPCSRF 57

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues  
al number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq.032802:\*

1:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT:*
2:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:*
3:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:*
4:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT:*
5:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT:*
6:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT:*
7:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT:*
8:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT:*
9:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT:*
10:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT:*
11:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT:*
12:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT:*
13:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT:*
14:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT:*
15:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:*
16:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:*
17:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:*
18:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:*
19:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:*
20:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT:*
21:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:*
22:	/SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	100.0	57	20	AAZ21862 Human agouti-relat
2	336	100.0	83	20	AAZ21861 Human agouti-relat
3	336	100.0	118	20	AAZ21856 Human agouti-relat
4	336	100.0	120	20	AAZ21857 Human agouti-relat
5	336	100.0	121	20	AAZ21858 Human agouti-relat
6	336	100.0	132	19	AAW26777 Human agouti-relat
7	336	100.0	132	19	AAW26780 Human agouti-relat
8	336	100.0	132	20	AAW49102 Human agouti-relat
9	336	100.0	132	21	AAW75125 Human agouti-relat
10	336	100.0	132	22	AAW75125 Human agouti-relat
11	336	100.0	605	20	AAZ21870 Amino acid sequenc

12	336	100.0	621	20	AAZ21874 Amino acid sequenc
13	336	100.0	622	20	AAZ21872 Amino acid sequenc
14	336	100.0	654	20	AAZ21859 Amino acid sequenc
15	336	100.0	666	20	AAZ21871 Amino acid sequenc
16	336	100.0	684	20	AAZ21873 Amino acid sequenc
17	336	100.0	684	20	AAZ21875 Amino acid sequenc
18	336	100.0	715	20	AAZ21860 Amino acid sequenc
19	321	95.5	54	19	AAW26778 Human agouti-relat
20	314	93.5	111	20	AAZ28598 Chimeric Leu127Pro
21	304	90.5	57	20	AAZ21864 Mouse agouti-relat
22	304	90.5	83	20	AAZ21863 Mouse agouti-relat
23	304	90.5	113	20	AAZ21866 Amino acid sequenc
24	304	90.5	117	20	AAZ21867 Amino acid sequenc
25	304	90.5	118	20	AAZ21865 Amino acid sequenc
26	304	90.5	131	20	AAW49104 Mouse agouti-relat
27	304	90.5	620	20	AAZ21868 Amino acid sequenc
28	304	90.5	683	20	AAZ21869 Amino acid sequenc
29	299	89.0	50	20	AAZ33951 Melanocortin-1 rec
30	298	88.7	131	19	AAW26779 Mouse agouti-relat
31	286	85.1	48	21	AAW26779 Human agouti-relat
32	281	83.6	46	20	AAW49101 Human agouti-relat
33	281	83.6	46	22	AAW49101 Human agouti-relat
34	271	80.7	46	20	AAW49103 Human agouti-relat
35	264.5	78.7	129	21	AAZ33593 Human agouti-relat
36	202	60.1	33	22	AAZ33593 Human agouti-relat
37	181	53.9	32	21	AAW00082 Agouti related pep
38	180	53.6	32	21	AAW00082 Agouti related pep
39	162	48.2	32	21	AAW00089 Agouti related pep
40	159	47.3	32	21	AAW00083 Agouti related pep
41	159	47.3	32	21	AAW00084 Agouti related pep
42	158	47.3	32	21	AAW00085 Agouti related pep
43	158	47.0	32	21	AAW00090 Agouti related pep
44	158	47.0	32	21	AAW00091 Agouti related pep
45	121.5	36.2	131	18	AAW10101 Murine agouti sign

## ALIGNMENTS

RESULT 1

AAZ21862 standard; protein; 57 AA.

AAZ21862:

20-SEP-1999 (first entry)

Human agouti-related transcript (ARF) protein.

ARF; agouti-related transcript; melanocyte stimulating hormone; MSH; melanocortin receptor; allosteric enhancer; obesity regulator.

Homo sapiens.

W09931508-A1.

24-JUN-1999.

11-DEC-1998; 98WO-US26457.

16-DEC-1997; 97US-0069747.

(MERI ) MERCK & CO INC.

Pong TM, Tota MR, Van Der Ploeg LHT;

WPI; 1999-430057/36.

Inhibiting binding of melanocyte stimulating hormones to melanocortin receptors

Claim 1; Page 7; 53pp; English.

CC The invention provides novel polypeptides derived from the C-terminal  
CC region of human and mouse agouti-related transcript (ART) protein. These  
CC peptides can be used to inhibit binding of melanocyte stimulating  
CC hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
CC of fusion proteins which have an amino acid sequence from the ART  
CC protein fused at its carboxy terminus to one or more amino acid sequences  
CC not derived from the ART protein. The ART polypeptides can be used to  
CC identify inhibitors and allosteric enhancers of the binding of the ART  
CC polypeptide to melanocortin receptors. The ART protein is also a  
CC regulator of human obesity, and substances that potentiate the effect of  
CC the ART protein on melanocortin receptors are likely to be of value in  
CC the control of body weight. Sequences AAY21861-863 represent specific  
CC examples of ART polypeptides that can be used in the invention. The  
CC present sequence represents a human ART protein fragment.

XX Sequence 57 AA:

Query Match 100.0%; Score 336; DB 20; Length 57;  
Best Local Similarity 100.0%; Pred. No. 7e-29;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDREPRSSRCVRLHESCLGQVPCDPCATCYCRFFNAFCYCRKLTGTAMNCSRT 57  
|||||  
DB 1 ldreprssrrcrllhescslgqgvpcdpcatcyrcrffnafcyckrlgtamncsrt 57

RESULT 2

AAY21861  
ID AAY21861 standard; protein; 83 AA.

XX AAY21861;

DT 20-SEP-1999 (first entry)

XX Human agouti-related transcript (ART) protein.

XX ART: agouti-related transcript; melanocyte stimulating hormone; MSH;  
XX melanocortin receptor; allosteric enhancer; obesity regulator.

XX Homo sapiens.

XX WO931508-A1.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-US26457.

XX 16-DEC-1997; 97US-0069747.

XX (MERI) MERCK & CO INC.

XX Fong TM, Tota MR, Van Der Ploeg LHT;

XX WPI: 1999-430057/36.

XX Inhibiting binding of melanocyte stimulating hormones to  
XX melanocortin receptors

XX Claim 1; Page 7; 53pp: English.

XX The invention provides novel polypeptides derived from the C-terminal  
XX region of human and mouse agouti-related transcript (ART) protein. These  
XX peptides can be used to inhibit binding of melanocyte stimulating  
XX hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
XX of fusion proteins which have an amino acid sequence from the ART  
XX protein fused at its carboxy terminus to one or more amino acid sequences  
XX not derived from the ART protein. The ART polypeptides can be used to  
XX identify inhibitors and allosteric enhancers of the binding of the ART  
XX polypeptide to melanocortin receptors. The ART protein is also a  
XX regulator of human obesity, and substances that potentiate the effect of  
XX the ART protein on melanocortin receptors are likely to be of value in  
XX the control of body weight. Sequences AAY21861-863 represent specific

CC examples of ART polypeptides that can be used in the invention. The  
CC present sequence represents a human ART protein fragment.

XX Sequence 83 AA;

Query Match 100.0%; Score 336; DB 20; Length 83;  
Best Local Similarity 100.0%; Pred. No. 9.8e-29;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDREPRSSRCVRLHESCLGQVPCDPCATCYCRFFNAFCYCRKLTGTAMNCSRT 57  
|||||  
DB 27 ldreprssrrcrllhescslgqgvpcdpcatcyrcrffnafcyckrlgtamncsrt 83

RESULT 3

AAY21856  
ID AAY21856 standard; protein; 118 AA.

XX AAY21856;

DT 20-SEP-1999 (first entry)

XX Amino acid sequence of fusion protein c-ART-a.

XX ART: agouti-related transcript; melanocyte stimulating hormone; MSH;  
XX melanocortin receptor; allosteric enhancer; obesity regulator.

XX Synthetic.

XX Homo sapiens.

XX WO931508-A1.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-US26457.

XX 16-DEC-1997; 97US-0069747.

XX (MERI) MERCK & CO INC.

XX Fong TM, Tota MR, Van Der Ploeg LHT;

XX WPI: 1999-430057/36.

XX Inhibiting binding of melanocyte stimulating hormones to  
XX melanocortin receptors

XX Claim 2; Page 4; 53pp: English.

XX The invention provides novel polypeptides derived from the C-terminal  
XX region of human and mouse agouti-related transcript (ART) protein. These  
XX peptides can be used to inhibit binding of melanocyte stimulating  
XX hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
XX of fusion proteins which have an amino acid sequence from the ART  
XX protein fused at its carboxy terminus to one or more amino acid sequences  
XX not derived from the ART protein. The ART polypeptides can be used to  
XX identify inhibitors and allosteric enhancers of the binding of the ART  
XX polypeptide to melanocortin receptors. The ART protein is also a  
XX regulator of human obesity, and substances that potentiate the effect of  
XX the ART protein on melanocortin receptors are likely to be of value in  
XX the control of body weight. Sequences AAY21861-863 represent specific  
XX examples of ART polypeptides that can be used in the invention. The  
XX present sequence represents a fusion protein containing the ART protein.

XX Sequence 118 AA;

Query Match 100.0%; Score 336; DB 20; Length 118;  
Best Local Similarity 100.0%; Pred. No. 1.3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LDREPRSSRCVRLHESCLGQVPCDPCATCYCRFFNAFCYCRKLTGTAMNCSRT 57

Db 32 lqdeprssrrcvrlhescclgqyvcddpcatcyctffnatcyckrkigtampcst 88

RESULT 4

AAV21857 standard; protein: 120 AA.

AAV21857;

20-SEP-1999 (first entry)

Amino acid sequence of fusion protein c-ART-b.

ART; agouti-related transcript; melanocyte stimulating hormone; MSH; melanocortin receptor; allosteric enhancer; obesity regulator.

Synthetic.

Homo sapiens.

MO9931508-A1.

24-JUN-1999.

11-DEC-1998; 98MO-US26457.

16-DEC-1997; 97US-0069747.

(MERI) MERCK & CO INC.

Fong TM, Tota MR, Van Der Ploeg LHT;

WPI: 1999-430057/36.

Inhibiting binding of melanocyte stimulating hormones to melanocortin receptors

Claim 2; Page 4; 53pp: English.

The invention provides novel polypeptides derived from the C-terminal region of human and mouse agouti-related transcript (ART) protein. These peptides can be used to inhibit binding of melanocyte stimulating hormones (MSHs) to melanocortin receptors. The ART proteins form a part of fusion proteins which have an amino acid sequence from the ART protein fused at its carboxy terminus to one or more amino acid sequences not derived from the ART protein. The ART polypeptides can be used to identify inhibitors and allosteric enhancers of the binding of the ART polypeptide to melanocortin receptors. The ART protein is also a regulator of human obesity, and substances that potentiate the effect of the ART protein on melanocortin receptors are likely to be of value in the control of body weight. Sequences AAV21861-863 represent specific examples of ART polypeptides that can be used in the invention. The present sequence represents a fusion protein containing the ART protein.

Sequence 120 AA;

Query Match 100.0%; Score 336; DB 20; Length 120; Best Local Similarity 100.0%; Pred. No. 1.4e-28; Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDEPRSSRRCVRLHESCCLGQVPCDDPCATCYCTFFNATCYCKRKIGTAMPSCST 57  
27 lqdeprssrrcvrlhescclgqyvcddpcatcyctffnatcyckrkigtampcst 83

RESULT 5

AAV21858 standard; protein: 121 AA.

AAV21858;

20-SEP-1999 (first entry)

Amino acid sequence of fusion protein c-ART-c.

ART; agouti-related transcript; melanocyte stimulating hormone; MSH; melanocortin receptor; allosteric enhancer; obesity regulator.

Synthetic.

Homo sapiens.

MO9931508-A1.

24-JUN-1999.

11-DEC-1998; 98MO-US26457.

16-DEC-1997; 97US-0069747.

(MERI) MERCK & CO INC.

Fong TM, Tota MR, Van Der Ploeg LHT;

WPI: 1999-430057/36.

Inhibiting binding of melanocyte stimulating hormones to melanocortin receptors

Claim 2; Page 5; 53pp: English.

The invention provides novel polypeptides derived from the C-terminal region of human and mouse agouti-related transcript (ART) protein. These peptides can be used to inhibit binding of melanocyte stimulating hormones (MSHs) to melanocortin receptors. The ART proteins form a part of fusion proteins which have an amino acid sequence from the ART protein fused at its carboxy terminus to one or more amino acid sequences not derived from the ART protein. The ART polypeptides can be used to identify inhibitors and allosteric enhancers of the binding of the ART polypeptide to melanocortin receptors. The ART protein is also a regulator of human obesity, and substances that potentiate the effect of the ART protein on melanocortin receptors are likely to be of value in the control of body weight. Sequences AAV21861-863 represent specific examples of ART polypeptides that can be used in the invention. The present sequence represents a fusion protein containing the ART protein.

Sequence 121 AA;

Query Match 100.0%; Score 336; DB 20; Length 121; Best Local Similarity 100.0%; Pred. No. 1.4e-28; Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDEPRSSRRCVRLHESCCLGQVPCDDPCATCYCTFFNATCYCKRKIGTAMPSCST 57  
27 lqdeprssrrcvrlhescclgqyvcddpcatcyctffnatcyckrkigtampcst 83

RESULT 6

AAW26777 standard; protein: 132 AA.

AAW26777;

08-JUN-1998 (first entry)

Human agouti-regulated protein ART.

Agouti-regulated gene; ART; human; melanocortin receptor; feeding behavior; food uptake; neuroendocrine disorder;

endocrine disorder; glucocorticoid resistance; Cushing's syndrome; congenital adrenal hyperplasia; obesity.

Homo sapiens.

Key Location/Qualifiers

Peptide 1.20  
/label= Sig\_peptide

W09743412-A1

20-NOV-1997.

22-APR-1997; 97WO-US06853.

27-NOV-1996; 96US-0757541.

10-MAY-1996; 96US-0017505.

(AMGE-) AMGEN INC.

Luethy R, Stark KL;

WPI: 1998-008881/01.

N-PSDB; AAT99565-67.

Nucleic acid molecule encoding agouti related polypeptide - useful to increase food uptake in mammal, and in the treatment of (neuro)endocrine disorders

Claim 26; Page 53-54; 77pp; English.

This protein comprises the novel human agouti-related polypeptide ART. Its amino acid sequence can be deduced from ART genomic DNA and cDNA clones (see AAT99565-67). A polymorphic variant (see AAT99567) of human ART has also been identified, as well as mouse ART (see AAT99567/9). Recombinant ART polypeptides, including a truncated human ART (see AAT99567/8), can be expressed in host cells. They can be used in a claimed method of increasing food uptake in mammals. The ART polypeptides may also be useful as modulators, or to prepare antibodies, of ART receptors in vitro or in vivo, e.g. inhibitors or stimulants, and may be employed in the treatment of endocrine and/or neuro-endocrine disorders, e.g. glucocorticoid resistance, Cushing's syndrome, congenital adrenal hyperplasia, other disorders of the hypothalamic-pituitary axis and/or obesity.

Sequence 132 AA;

Query Match 100.0%; Score 336; DB 19; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDRPSSRRRCVRLHESCLGQVPCDCPCATCYCRFFNAFCRKLGTAMNCSRT 57  
76 LQDRPSSRRRCVRLHESCLGQVPCDCPCATCYCRFFNAFCRKLGTAMNCSRT 132

RESULT 7

AAW26780 AAW26780 standard; Protein; 132 AA.

AC AAW26780;

08-JUN-1998 (first entry)

Human agouti-related protein ART variant.

Agouti-regulated gene; ART; human; melanocortin receptor; feeding behavior; food uptake; neuroendocrine disorder; endocrine disorder; glucocorticoid resistance; Cushing's syndrome; congenital adrenal hyperplasia; obesity.

Homo sapiens.

Key Location/Qualifiers  
Reptide 1.20 /label= Sig\_peptide

W09743412-A1.

20-NOV-1997.

22-APR-1997; 97WO-US06853.

27-NOV-1996; 96US-0757541.

10-MAY-1996; 96US-0017505.

(AMGE-) AMGEN INC.

Luethy R, Stark KL;

WPI: 1998-008881/01.

Nucleic acid molecule encoding agouti related polypeptide - useful to increase food uptake in mammal, and in the treatment of (neuro)endocrine disorders

Claim 26; Page 56-57; 77pp; English.

This protein comprises the novel human agouti-related polypeptide, ART. It arises from a polymorphism identified in some sequenced ART cDNA clones; other ART polypeptides (see AAT99567/7) have leucine rather than proline at amino acid position 45. ART polypeptides (see AAT99567/8) can be expressed in host cells and used in a claimed method of increasing food uptake in mammals. They may also be useful as modulators, e.g. inhibitors or stimulants, of ART receptors in vitro or in vivo, or to prepare antibodies, and may be employed in the treatment of endocrine and/or neuro-endocrine disorders, e.g. glucocorticoid resistance, Cushing's syndrome, congenital adrenal hyperplasia, other disorders of the hypothalamic-pituitary axis and/or obesity.

Sequence 132 AA;

Query Match 100.0%; Score 336; DB 19; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LQDRPSSRRRCVRLHESCLGQVPCDCPCATCYCRFFNAFCRKLGTAMNCSRT 57  
76 LQDRPSSRRRCVRLHESCLGQVPCDCPCATCYCRFFNAFCRKLGTAMNCSRT 132

RESULT 8

AA49102 AAY49102 standard; Protein; 132 AA.

AC AAY49102;

17-JAN-2000 (first entry)

Human agouti-related protein (AGRP) amino acid sequence.

MARP; minimised agouti-related protein; agouti-related protein; AGRP; melanocortin receptor; neuropeptide; feeding behaviour; satiety signal; wasting syndrome; HTV; cachexia; anorexia; cancer; hypothalamic control.

Homo sapiens.

W09950295-A2.

07-OCT-1999.

30-MAR-1999; 99WO-US06968.

30-MAR-1998; 98US-0079957.

(GRYP-) GRYPHON SCI.

Thompson DA, Wilken J, Gantz I, Kent SBH;

DR WPI: 1999-610837/52.

XX New agouti-related protein analogues and their fragments, used for  
PT treating wasting syndromes, e.g. cachexia, and for drug screening  
XX  
PS Disclosure; Fig 1: 46pp; English.

CC This is the human agouti-related protein amino acid sequence (AGRP).  
CC AGRP is a natural antagonist of melanocortin receptors. The cysteine rich  
CC C-terminal region (AAV49101) of the protein folds independently and  
CC retains the activity of the full length protein. The AGRP neuropeptide is  
CC a major regulator of feeding behaviour, specifically it antagonizes the  
CC melanocortin receptor, making it impossible for the receptor to transmit  
CC a satiety signal. The invention relates to human and murine AGRP  
CC analogues and their fragments. The peptides of the invention can be used  
CC to treat wasting syndromes e.g. human immune deficiency virus wasting  
CC syndrome, or cancer-associated cachexia or anorexia. AGRP analogues can  
CC also be used for structure-function analysis of AGRP activity and to  
CC screen for agents that have (ant)agonistic activity at specific subtypes  
CC of melanocortin receptors, potentially useful for treating wasting  
CC syndromes, obesity or other disorders that involve hypothalamic control  
CC of feeding.

SO Sequence 132 AA;

Query Match 100.0%; Score 336; DB 20; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQDRPRSSNRRCVRLHESCLGQVPCDDPCATCYCRFPNFCYCRKLGTAAMPSCRT 57  
|||||  
DB 76 LQDREPRSSNRRCVRLHESCLGQVPCDDPCATCYCRFPNFCYCRKLGTAAMPSCRT 132

#### RESULT 9

AAV83186  
ID AAV83186 standard; peptide; 132 AA.

XX AAV83186;

DT 24-JUL-2000 (first entry)

XX Melanocortin receptor MC4 receptor ligand AGRP.

DE Membrane polypeptide; lipid matrix; synthesis; ligation;  
XX chemoselective ligation; fluorescence resonance energy transfer;  
KW FRER; chromophore; ligand; receptor domain; drug screening;  
TW diagnosis; ion channel; melanocortin receptor; MC4; AGRP.

OS Synthetic.

OS Homo sapiens.

XX W0200012536-A2.

PN 09-MAR-2000.

PD 26-AUG-1999; 99WO-US19542.

PE 31-AUG-1998; 98US-0144964.

PR 05-MAR-1999; 99US-0263971.

XX (GRYP-) GRYPHON SCI.

XX Kochoenderfer GG, Hunter CL, Kent SBH, Botti P;

PI WPI: 2000-270792/23.

DR Selectively labeled membrane peptides, useful e.g. for detecting ligand  
XX binding to receptors and in drug screening, are prepared, in lipid  
PT matrix, by reaction between amino acid residues  
XX  
PS Example 12; Page 71-72; 120pp; English.

XX New methods are described by which membrane polypeptides can be  
CC labelled. The method comprises chemoselective chemical ligation of  
CC the membrane polypeptide which is incorporated in a lipid matrix,  
CC and a ligation label. Both contain an amino acid having an  
CC unprotected reactive group that together undergo chemoselective  
CC ligation to form a covalent bond. The method can be used to label  
CC folded polypeptides embedded in a lipid membrane, by treating the  
CC polypeptide with a reagent that cleaves specifically adjacent to an  
CC amino acid with an unprotected reactive group and then ligating the  
CC cleaved polypeptide with the ligation label. The ligation label can  
CC be a chromophore, thus ligand binding to membrane bound polypeptides  
CC can be detected by contacting a membrane bound polypeptide comprising  
CC a chromophore, with the ligand under investigation and screening for  
CC binding in an assay characterized by detecting fluorescence resonance  
CC energy transfer (FRET) between the chromophore and a second  
CC chromophore, the chromophores comprising a donor and acceptor pair of  
CC a resonance energy transfer system. The methods are used for lipid  
CC matrix-assisted chemical ligation and synthesis of membrane  
CC polypeptides. Labeled membrane polypeptides are used to detect ligand  
CC binding and the identification of receptor domains, e.g. for  
CC structure/activity studies. They can also be used in drug screening,  
CC selection or design, and for diagnosis. The methods are particularly  
CC used for fluorescent resonance energy transfer (FRET) analysis of  
CC previously inaccessible membrane polypeptides. The method allows  
CC site-specific incorporation of labels during polypeptide synthesis  
CC and analysis of previously inaccessible membrane proteins. A  
CC Melanocortin receptor MC4 which also comprises a Factor Xa cleavage  
CC site (AAV83182) can be cleaved with Factor Xa to give a  
CC C-terminal alpha-thioester modified MC4 receptor ligation label  
CC (AAV83183) and an MC4 receptor membrane polypeptide cleavage product  
CC (AAV83184). Chemical ligation of cleaved MC4 in alternative  
CC membrane patches or micelles to an MC4 ligation label produces the  
CC synthetic labeled MC4 product (AAV83185). FRET analysis of the  
CC labeled MC4 product and the MC4 receptor ligand AGRP which is  
CC labeled with TAMRA (paired with Tb+3 chelate) or TEXAS RED (paired  
CC with Eu+3 chelate).

SO Sequence 132 AA;

Query Match 100.0%; Score 336; DB 21; Length 132;  
Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQDRPRSSNRRCVRLHESCLGQVPCDDPCATCYCRFPNFCYCRKLGTAAMPSCRT 57  
|||||  
DB 76 LQDREPRSSNRRCVRLHESCLGQVPCDDPCATCYCRFPNFCYCRKLGTAAMPSCRT 132

#### RESULT 10

AAV75125  
ID AAV75125 standard; protein; 132 AA.

XX AAV75125;

DT 01-AUG-2001 (first entry)

XX Human agouti related protein (AGRP) SEQ ID NO:1.

DE Human; agouti related protein; AGRP; minimised agouti related protein;  
XX MAMP; MAMP-33; melanocortin receptor-ligand binding; wasting syndrome;  
KW MAMP co-ordinate data; feeding behaviour.

XX Homo sapiens.

XX W0200130808-A1.

PN 03-MAY-2001.

PF 27-OCT-1999; 99WO-US25201.

PR 27-OCT-1999; 99WO-US25201.  
 XX (RSGC ) UNIV CALIFORNIA.  
 XX  
 PA Millhauser GL, Bolin KA, Anderson DJ;  
 P1 WPI; 2001-316321/33.  
 DR  
 XX

Methods and compounds for modulating melanocortin receptor-ligand binding are useful for treating wasting syndromes

Example 1; Page 51; 53pp; English.

The present invention describes a method of identifying a compound that modulates ligand binding to a melanocortin receptor. The method comprises modelling test compounds to fit spatially into the binding site, screening the compounds in a binding assay for the binding site and identifying compounds that modulate the ligand binding. Also described are: (1) a machine-readable data storage medium able to display a graphical three-dimensional representation of a molecule that binds a melanocortin receptor comprising structure co-ordinates of amino acid residues corresponding to residues 1-18 of the N-terminal loop, residues 19-34 of the central loop and residues 35-46 of the C-terminal loop of the minimised agouti related protein (MARP) or a homologue; (2) a machine-readable data storage medium comprising a Fourier transform of at least a portion of the structural co-ordinates of the receptor and an X-ray diffraction pattern of the molecule; (3) an NMR structure of the MARP embodied in a computer readable medium; (4) compounds identified by the method; (5) a polypeptide comprising the sequence further mislaminisation of human agouti related protein (AGRP) designated MARP-33 (1); (6) a method of treating disease comprising administration of the polypeptide (1); and (7) compositions comprising (1). (1) are useful for treating wasting syndromes. AGRP plays a major role in the regulation of mammalian feeding behaviour. The present sequence represents human AGRP.

Sequence 132 AA;

Query Match 100.0%; Score 336; DB 22; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-28;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDRPSSRRKVRHESCLGQOVPCPCPCATCYCFNFATCYCKRLGTAMPSCRT 57  
 DB 76 LQDRPSSRRKVRHESCLGQOVPCPCPCATCYCFNFATCYCKRLGTAMPSCRT 132

RESULT 11

AAV21870 standard; protein: 605 AA.

AAV21870;

20-SEP-1999 (first entry)

Amino acid sequence of fusion protein containing ART protein.

ART; agouti-related transcript; melanocyte stimulating hormone; MSH;  
 melanocortin receptor; allosteric enhancer; obesity regulator.

Synthetic.  
 Homo sapiens.

W09931508-A1.

24-JUN-1999.

11-DEC-1998; 98WO-US26457.

16-DEC-1997; 97US-0069747.

(MERI ) MERCK & CO INC.

PI Fong TM, Tota MR, Van Der Ploeg LHT;  
 DR WPI; 1999-430057/36.  
 XX  
 XX  
 PT Inhibiting binding of melanocyte stimulating hormones to  
 PT melanocortin receptors  
 XX  
 PS Claim 2; Page 11-12; 53pp; English.

The invention provides novel polypeptides derived from the C-terminal region of human and mouse agouti-related transcript (ART) protein. These peptides can be used to inhibit binding of melanocyte stimulating hormones (MSHs) to melanocortin receptors. The ART proteins form a part of fusion proteins which have an amino acid sequence from the ART protein fused at its carboxy terminus to one or more amino acid sequences not derived from the ART protein. The ART polypeptides can be used to identify inhibitors and allosteric enhancers of the binding of the ART polypeptide to melanocortin receptors. The ART protein is also a regulator of human obesity, and substances that potentiate the effect of the ART protein on melanocortin receptors are likely to be of value in the control of body weight. Sequences AAV21861-863 represent specific examples of ART polypeptides that can be used in the invention. The present sequence represents a fusion protein containing the ART protein.

Sequence 605 AA;

Query Match 100.0%; Score 336; DB 20; Length 605;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-28;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDRPSSRRKVRHESCLGQOVPCPCPCATCYCFNFATCYCKRLGTAMPSCRT 57  
 DB 27 LQDRPSSRRKVRHESCLGQOVPCPCPCATCYCFNFATCYCKRLGTAMPSCRT 83

RESULT 12

AAV21874 standard; protein: 621 AA.

AAV21874;

20-SEP-1999 (first entry)

Amino acid sequence of fusion protein containing ART protein.

ART; agouti-related transcript; melanocyte stimulating hormone; MSH;  
 melanocortin receptor; allosteric enhancer; obesity regulator.

Synthetic.  
 Homo sapiens.

W09931508-A1.

24-JUN-1999.

11-DEC-1998; 98WO-US26457.

16-DEC-1997; 97US-0069747.

(MERI ) MERCK & CO INC.

Fong TM, Tota MR, Van Der Ploeg LHT;

WPI; 1999-430057/36.

Inhibiting binding of melanocyte stimulating hormones to  
 melanocortin receptors

Claim 2; Page 16; 53pp; English.

The invention provides novel polypeptides derived from the C-terminal region of human and mouse agouti-related transcript (ART) protein. These

CC peptides can be used to inhibit binding of melanocyte stimulating  
 CC hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
 CC of fusion proteins which have an amino acid sequence from the ART  
 CC protein fused at its carboxy terminus to one or more amino acid sequences  
 CC not derived from the ART protein. The ART polypeptides can be used to  
 CC identify inhibitors and allosteric enhancers of the binding of the ART  
 CC polypeptide to melanocortin receptors. The ART protein is also a  
 CC regulator of human obesity, and substances that potentiate the effect of  
 CC the ART protein on melanocortin receptors are likely to be of value in  
 CC the control of body weight. Sequences AAY21861-863 represent specific  
 CC examples of ART polypeptides that can be used in the invention. The  
 CC present sequence represents a fusion protein containing the ART protein.  
 XX  
 SQ Sequence 621 AA:

Query Match 100.0%; Score 336; DB 20; Length 621;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-28;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LODRPRSSRRVCRLHESCLGQVPCDCPCATCYCFRFAFCYCRKLGTMNPSRT 57  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 565 lqdrprssrrvcrlhesclgqgvpcdcpcatcyccrfnafcyckrlgtamncsrt 621

## RESULT 13

AAY21872  
 ID AAY21872 standard; protein; 622 AA.

XX AAY21872;

DT 20-SEP-1999 (first entry)

XX Amino acid sequence of fusion protein containing ART protein.

XX ART: agouti-related transcript; melanocyte stimulating hormone; MSH;  
 XX melanocortin receptor; allosteric enhancer; obesity regulator.

XX Synthetic.

OS Homo sapiens.

XX WO9931508-A1.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-US26457.

XX 16-DEC-1997; 97US-0069747.

XX (MERI ) MERCK & CO INC.

XX Fong TM, Tota MR, Van Der Ploeg LHT;

XX WPT; 1999-430057/36.

XX Inhibiting binding of melanocyte stimulating hormones to  
 XX melanocortin receptors  
 XX 1

PS Claim 2; Page 13-14; 53pp; English.

XX The invention provides novel polypeptides derived from the C-terminal  
 CC region of human and mouse agouti-related transcript (ART) protein. These  
 CC peptides can be used to inhibit binding of melanocyte stimulating  
 CC hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
 CC of fusion proteins which have an amino acid sequence from the ART  
 CC protein fused at its carboxy terminus to one or more amino acid sequences  
 CC not derived from the ART protein. The ART polypeptides can be used to  
 CC identify inhibitors and allosteric enhancers of the binding of the ART  
 CC polypeptide to melanocortin receptors. The ART protein is also a  
 CC regulator of human obesity, and substances that potentiate the effect of  
 CC the ART protein on melanocortin receptors are likely to be of value in  
 CC the control of body weight. Sequences AAY21861-863 represent specific  
 CC examples of ART polypeptides that can be used in the invention. The

CC present sequence represents a fusion protein containing the ART protein.  
 XX  
 SQ Sequence 622 AA:

Query Match 100.0%; Score 336; DB 20; Length 622;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-28;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODRPRSSRRVCRLHESCLGQVPCDCPCATCYCFRFAFCYCRKLGTMNPSRT 57  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 76 lqdrprssrrvcrlhesclgqgvpcdcpcatcyccrfnafcyckrlgtamncsrt 132

## RESULT 14

AAY21859  
 ID AAY21859 standard; protein; 654 AA.

XX AAY21859;

DT 20-SEP-1999 (first entry)

XX Amino acid sequence of fusion protein ART-AP.

XX ART: agouti-related transcript; melanocyte stimulating hormone; MSH;  
 XX melanocortin receptor; allosteric enhancer; obesity regulator.

XX Synthetic.

OS Homo sapiens.

XX WO9931508-A1.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-US26457.

XX 16-DEC-1997; 97US-0069747.

XX (MERI ) MERCK & CO INC.

XX Fong TM, Tota MR, Van Der Ploeg LHT;

XX WPT; 1999-430057/36.

XX Inhibiting binding of melanocyte stimulating hormones to  
 XX melanocortin receptors  
 XX Claim 2; Page 5-6; 53pp; English.

XX The invention provides novel polypeptides derived from the C-terminal  
 CC region of human and mouse agouti-related transcript (ART) protein. These  
 CC peptides can be used to inhibit binding of melanocyte stimulating  
 CC hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
 CC of fusion proteins which have an amino acid sequence from the ART  
 CC protein fused at its carboxy terminus to one or more amino acid sequences  
 CC not derived from the ART protein. The ART polypeptides can be used to  
 CC identify inhibitors and allosteric enhancers of the binding of the ART  
 CC polypeptide to melanocortin receptors. The ART protein is also a  
 CC regulator of human obesity, and substances that potentiate the effect of  
 CC the ART protein on melanocortin receptors are likely to be of value in  
 CC the control of body weight. Sequences AAY21861-863 represent specific  
 CC examples of ART polypeptides that can be used in the invention. The  
 CC present sequence represents a fusion protein containing the ART protein  
 CC and an alkaline phosphatase protein.

SQ Sequence 654 AA:

Query Match 100.0%; Score 336; DB 20; Length 654;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-28;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODRPRSSRRVCRLHESCLGQVPCDCPCATCYCFRFAFCYCRKLGTMNPSRT 57

Db 76 lqdrepsrrrcvrlhescslgqgvpccdpccatcyrcrfnafcyckrlgtampscrt 132

## RESULT 15

ID AAY21871 standard; protein: 666 AA.

AC AAY21871;

DF 20-SEP-1999 (first entry)

DE Amino acid sequence of fusion protein containing ART protein.

KM ART; agouti-related transcript; melanocyte stimulating hormone; MSH;  
KW melanocortin receptor; allosteric enhancer; obesity regulator.

OS Synthetic.

OS Homo sapiens.

WO9931508-A1.

24-JUN-1999.

11-DEC-1998; 98WO-US26457.

16-DEC-1997; 97US-0069747.

(MERI ) MERCK & CO INC.

Fong TM, Tota MR, Van Der Ploeg LHT;

WPI: 1999-430057/36.

PT Inhibiting binding of melanocyte stimulating hormones to  
melanocortin receptors

Claim 2; Page 12-13; 53pp; English.

CC The invention provides novel polypeptides derived from the C-terminal  
CC region of human and mouse agouti-related transcript (ART) protein. These  
CC peptides can be used to inhibit binding of melanocyte stimulating  
CC hormones (MSHs) to melanocortin receptors. The ART proteins form a part  
CC of fusion proteins which have an amino acid sequence from the ART  
CC protein fused at its carboxy terminus to one or more amino acid sequences  
CC not derived from the ART protein. The ART polypeptides can be used to  
CC identify inhibitors and allosteric enhancers of the binding of the ART  
CC polypeptide to melanocortin receptors. The ART protein is also a  
CC regulator of human obesity, and substances that potentiate the effect of  
CC the ART protein on melanocortin receptors are likely to be of value in  
CC the control of body weight. Sequences AAY21861-863 represent specific  
CC examples of ART polypeptides that can be used in the invention. The  
CC present sequence represents a fusion protein containing the ART protein.

SO Sequence 666 AA:

Query Match 100.0%; Score 336; DB 20; Length 666;  
Best Local Similarity 100.0%; Pred. No. 6,3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQDREPSRRRCVRLHESCLGQGVPCCDPCATCYRCRFNFCYCKRLGTAMPSCRT 57  
DB 27 LQDREPSRRRCVRLHESCLGQGVPCCDPCATCYRCRFNFCYCKRLGTAMPSCRT 83

Search completed: July 22, 2002, 17:18:34  
Job time: 349 sec



GenCore version 4.5.1  
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OM protein - protein search, using sw model

Run on: July 22, 2002, 17:13:45 ; Search time 18.36 Seconds

(without alignments)  
298.317 Million cell updates/sec

Title: US-09-581-894A-7

Perfect score: 336

Sequence: 1 LQDRPSSSRRCVRLHESCL.....FNAPFCRLGTRMPCSRF 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Minimum number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	121.5	36.2	131	2	A46298 pigment deposition
2	119.5	35.4	132	2	A37743 agouti protein pre
3	84.5	25.1	46	2	B53613 plectoxin VIII - s
4	84.5	25.1	46	2	F53613 plectoxin XI - sp
5	82.5	24.6	46	2	C53613 plectoxin XII - sp
6	82	24.4	45	2	D53613 plectoxin V - spid
7	82	24.4	46	2	A53613 plectoxin alpha-1 ch
8	70.5	21.0	3712	2	S18253 testis-specific pr
9	67.5	20.1	63	2	S25772 probable zinc meta
10	66.5	19.8	512	2	T37819 serine proteinase
11	66	19.6	118	2	S01140 keratin high-sulfu
12	66	19.6	1548	2	S34583 outer dense fiber
13	65.5	19.5	131	1	KRSH43 LIM homeobox prote
14	65.5	19.5	132	1	KRG737 proteinase inhibitor
15	65	19.3	247	2	I48699 phospholipase A2 (
16	63.5	18.9	348	2	T34266 F-spondin - rat
17	63	18.8	250	2	S71522 outer dense fiber
18	62.5	18.6	81	1	FTZB2 proteinase inhibitor
19	62	18.5	118	1	PSL74E phospholipase A2 (
20	62	18.5	807	2	A38152 F-spondin - rat
21	62	18.5	1487	2	G96827 protein P20B17.10
22	61.5	18.3	262	2	S56100 outer dense fiber
23	61.5	18.3	1119	2	A88481 protein C16A3.6 (1
24	61	18.2	137	2	A88481 phospholipase A2 (
25	61	18.2	151	2	T30032 hypothetical prote
26	61	18.2	1170	1	TSHUP1 thrombospondin 1 p
27	60.5	18.0	164	2	A40558 hypothetical prote
28	60.5	18.0	164	2	T24272 outer dense fiber
29	60.5	18.0	262	2	S56101

30	60.5	18.0	669	2	T06702 hypothetical prote
31	60	17.9	82	1	FTZB1 proteinase inhibitor
32	60	17.9	118	1	PSL73E phospholipase A2 (
33	60	17.9	122	1	PSR5A phospholipase A2 (
34	60	17.9	122	1	PSR5A phospholipase A2 (
35	60	17.9	122	2	A3317 phospholipase A2 (
36	60	17.9	371	2	T27637 hypothetical prote
37	60	17.9	633	2	T24898 hypothetical prote
38	60	17.9	650	2	H81708 hypothetical prote
39	59.5	17.7	68	2	S25775 testis-specific pr
40	59.5	17.7	188	2	T15651 testis-specific pr
41	59	17.6	56	1	WTFR hypothetical prote
42	59	17.6	118	2	JK0223 phospholipase A2 (
43	59	17.6	118	2	B34860 phospholipase A2 (
44	59	17.6	139	1	PSIV phospholipase A2 (
45	59	17.6	551	2	S07089 arylsulfatase (EC

#### ALIGNMENTS

RESULT 1  
A46298  
pigment deposition control protein agouti A precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 21-Sep-1993 #sequence, revision 18-Nov-1994 #text, change 28-Jul-2000  
C:Accession: A46298; A44330; I58127; I78534; I78535; B47318  
R:Miller, M.W.; Duhl, D.M.; Vrieling, H.; Cordes, S.P.; Ollmann, M.M.; Winkes, B.M.  
Genes Dev. 7, 454-467, 1993  
A:Title: Cloning of the mouse agouti gene predicts a secreted protein ubiquitously  
A:Reference number: A46298; MUID:93194064  
A:Accession: A46298  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-131 <MIL>  
A:Cross-references: GB:J06451; NID:9191797; PIDN:AAA37201.1; PID:9191798  
A:Experimental source: hair follicle  
A:Note: sequence extracted from NCBI backbone (NCBIN:127209, NCBI:127211)  
R:Bultman, S.J.; Michaud, E.J.; Woychik, R.P.  
Cell 71, 1195-1204, 1992  
A:Title: Molecular characterization of the mouse agouti locus.  
A:Reference number: A44330; MUID:93113687  
A:Contents: C3H  
A:Accession: A44330  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-131 <BUL>  
A:Cross-references: GB:J06941; NID:9191800  
A:Note: this translation is not annotated in GenBank entry MUSACT, release 111.0; s  
R:Duhl, D.M.; Vrieling, H.; Miller, K.A.; Wolff, G.L.; Barsh, G.S.  
Nature Genet. 8, 59-65, 1994  
A:Title: Neomorphic agouti mutations in obese yellow mice.  
A:Reference number: I58127; MUID:95078924  
A:Accession: I58127  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-16 <DUH1>  
A:Cross-references: GB:S74479; NID:9765284  
A:Experimental source: allele Avy  
A:Accession: I78534  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-16 <DUH2>  
A:Cross-references: GB:S74489; NID:9765282  
A:Experimental source: allele Aiy2  
A:Accession: I78535  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-16 <DUH3>  
A:Cross-references: GB:S74493; NID:9765281  
A:Experimental source: allele Aiy1  
R:Michaud, E.J.; Bultman, S.J.; Stubbs, L.J.; Woychik, R.P.  
Genes Dev. 7, 1203-1213, 1993

A:Accession: B47318  
A:Status: preliminary  
A:Molecule\_type: mRNA  
A:Residues: 1-70 <MIC>  
A:Cross\_references: GB:S63413; NID:g442169; PIDD:AA15908.1; PID:g442170  
A:Experimental\_source: spleen  
A:Note: sequence extracted from NCBI backbone (NCBIN:134705, NCBIPI:134706)  
C:Genetics:  
A:Gene: agouti  
C:Superfamily: agouti protein ASIP  
C:Keywords: glycoprotein; hair; hormone  
F:1-22/Domains: signal sequence #status predicted <SIG>  
F:23-131/Product: pigment deposition control protein agouti A #status predicted <MAT>  
F:39/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match Similarity      36.2%      Score 121.5:  DB 2:  length 131:
Best Local Similarity      34.8%      Pred. No. 6.5e-06:
Matches      23:  Conservative      8:  Mismatches      16:  Indels      19:  Gaps      2:

OY      3  DEPRSSRR-----CVRLESTGLGQGVPCCDPCATCYCRFFNAFCYCRKL 47
      ::  |||::      ||  ::||  |||||::|||::  ||  ||
DB      68  ERKRSKSKKAKMKVAPPPSPCVATRDSCKPPAPACCDPCASQCFRFSGACTCR-- 125
      48  GTANP 53
      :  ||
DB      126  --VLNP 129

```

```

RESULT      2
137143
Agouti protein precursor -- human
C:Species: Homo sapiens (man)
C:Date: 01-Mar-1996 #sequence_revision 01-Mar-1996 #text_change 28-Jul-2000
C:Accession: I37143
R:Kwon, H.Y.; Bultman, S.J.; Loeffler, C.; Chen, W.; Furdon, P.J.; Powell, J.G.; Usala, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 9760-9764, 1994
A>Title: Molecular structure and chromosomal mapping of the human homolog of the agouti
A:Reference number: I37143; MUID:95024040
A:Accession: I37143
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-132 <RES>
A:Cross-references: EMBL:U12775; NID:G540071; PIDN:AAB61247.1; PID:G540073
A:Genetics:
    Gene: GDB:ASIP
    Cross-references: GDB:392697; OMIM:600201
    Map position: 20q11.2-20q12
A:Introns: 54/1, 74/3
C:Superfamily: agouti protein ASIP

```

```

Query Match          35.4%: Score 119: DB 2: Length 132:
Best Local Similarity 50.0%: Pred. No. 1.2e-05:
Matches      22:  Conservative      3:  Mismatches 17:  Indels      2:  Gaps      1:

Oy      6  PRS--SRRCVRLHESCLGQVPCDCATCYCFRFPNACYCRKL  47
      ||:  |  ||  ||  |||||:|  |||:  |  ||  |
Db      85  PRTPLSAFCVATRNKCRPPAPACDCPCQCFRFRSACSCHVL  128

RESULT      3
B53613
PlectroIn VIII - spider (Plectreureys tristis).
C:Species: Plectreureys tristis
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Aug-1998
C:Accession: B53613
R:Oulstad, G.B.: Skinner, W.S.
J. Biol. Chem. 269, 11098-11101, 1994
A:Title: Isolation and sequencing of insecticidal peptides from the primitive hunting spider
A:Reference number: A53613; MUID:94209277

```

A;Accession: B53613  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-46 <OUT>  
C;Superfamily: curtatoxin

Query Match	-25.18	Score	84.5	DB	2	Length	46
Best Local Similarity	38.28	Pred. No.	0.024				
Matches	13	Conservative	5	Mismatches	15	Indels	1
						Gaps	1

```

0y      11 RCVRLHESCLGQVPPCCDPATCYCRFFNAFCYC 44
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      3 KCIGMQETCNG-KLPCCDGCVMCECNIMGQNCRC 35

```

RESULT 4  
F53613  
plectoxin XIV - spider (Plectreurys tristis)  
C:Species: Plectreurys tristis  
C:Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #extl\_change 21-Aug-1998  
C:Accession: F53613  
R:Ouistad, G.B.; Skinner, W.S.  
J Biol. Chem. 269, 11098-11101, 1994  
A:Title: Isolation and sequencing of insecticidal peptides from the primitive hantide from the primitive  
A:Reference number: A53613; M01D:94209277  
A:Accession: F53613  
A:Status: Preliminary  
A:Molecule type: protein  
A:Residues: 1-46 <Q07>  
C:Superfamily: curatloxin

Query Match	25.1%	Score	84.5	DB	2	Length	46
Best Local Similarity	38.2%	Pred. No.	0.024				
Matches	13	Conservative	5	Mismatches	15	Indels	1
						Gaps	1

```

QY      11 RCVRLHESCIQGVPPCCDPCATCYCRFFNAFCYC 44
      :|: | | :| | | | | | | | |
Db      3 KCIGMQETCNG-KLPCCDGCVMCECNIMQNCRC 35

```

RESULT 5  
C53613  
plectoxin XI - spider (Plectreurys tristis)  
C:Species: Plectreurys tristis  
C:date: 07-Jul-1995 #sequence\_rev1sion 07-Jul-1995 #text\_change 21-Aug-1998  
C:Accession: C53613  
R:Quistad, G.B.; Skinner, W.S.  
J. Biol. Chem. 269, 11098-11101, 1994  
A:Title: Isolation and sequencing of insecticidal peptides from the primitive hunter  
A:Reference number: A53613; MUID:94209277  
A:Accession: C53613  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-46 <QUT>  
C:Superfamily: curliatoxin

Query Match	24.6%	Score	82.5	DB	2	Length	46
Best Local Similarity	38.2%	Pred. No.	0.039				
Matches	13	Conservative	3	Mismatches	17	Indels	1
						Gaps	1

```

QY      11 RCVRLHESCLGQVPPCCDPACATCYCRFFNAFCYC 44
      :|: | | | :||| | | |
Db      3 KCIGMDEYCRG-NLPCCDDCVMECECNIMGQNCRC 35

```

```
RESULT 6
D53613
plectoxin XII - spider (Plectreurus tristis)
CtSpecies: Plectreurus tristis
CtDate: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 21-Aug-1996
```



submitted to the EMBL Data Library, August 1997

A:Reference number: Z21737  
 A:Accession: T37819  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-512 <DEV>  
 A:Cross-references: EMBL:Z98849; PIDN:CB11504.1; GSPDB:GN00066; SPDB:SPAC17A5.04C  
 A:Experimental source: strain 972h-; cosmid c17A5  
 A:Genetics:  
 A:Gene: SPDB:SPAC17A5.04C  
 A:Map position: 1  
 A:Introns: 316/1

Query Match 19.8%; Score 66.5; DB 2; Length 512;  
 Best Local Similarity 33.9%; Pred. No. 8.8;  
 Matches 19; Conservative 4; Mismatches 12; Indels 21; Gaps 5;

17 EAGLGGGVPCD-PC-----ATCY-CRFNAPCYCKIGTAMNCSR 56  
 333 EDC--KNNPCDCKTKTKTGSLCDQDQACCYCCHFNKAGTLCRO---STNCDK 383

RESULT 11

phospholipase A2 (EC 3.1.1.4) - yellow-lipped sea krait  
 C:Species: Laticauda colubrina (yellow-lipped sea krait)  
 C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 24-Jul-1997  
 C:Accession: S01140  
 R:Takasaka, C.; Kimura, S.; Kokubun, Y.; Tamiya, N.  
 A:Title: Isolation, properties and amino acid sequences of a phospholipase A2 and its ho  
 A:Reference number: S01140; MOID:89025636  
 A:Accession: S01140  
 A:Molecule type: protein  
 A:Residues: 1-118 <YAK>  
 C:Superfamily: phospholipase A2  
 C:Keywords: carboxylic ester hydrolase  
 F:48/92/Active site: His, Asp #status predicted

Query Match 19.6%; Score 66; DB 2; Length 118;  
 Best Local Similarity 27.1%; Pred. No. 3.8;  
 Matches 16; Conservative 3; Mismatches 16; Indels 24; Gaps 2;

11 RCVRHESCLGQOV-----PCDPCATCY-----CRFNAPCYCR 45  
 43 RCKRTDDPCGQAKKCGCFPLILYNFICRPGPTCDRGTTCRFVCDICDIAAFCAR 101

RESULT 12

serine protease (EC 3.4.21.-) PC6B - mouse  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 05-Nov-1999  
 C:Accession: S34583  
 R:Nakagawa, T.; Murakami, K.; Nakayama, K.  
 A:Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a  
 A:Reference number: S34583; MOID:93327934  
 A:Accession: S34583  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-1548 <NAK>  
 A:Cross-references: GB:D17583; NID:g407344; PIDN:BA04507.1; PID:d1005033; PID:g440374  
 C:Keywords: hydrolase, serine protease

Query Match 19.6%; Score 66; DB 2; Length 1548;  
 Best Local Similarity 29.6%; Pred. No. 20;  
 Matches 21; Conservative 2; Mismatches 28; Indels 20; Gaps 4;

2 QDRPNSSRCVRLHESCLG---QGVPCDPCATCYCRFNAPCY-----CR 45

Db 701 QDSE---YECMPCDEBCLCTEDDEPACTSCATGX-YMFERHCYKACPERFVGWKECR 756  
 Oy 46 KLGATAMNCSR 56  
 Db 757 ACCTGCGSCDQ 767

RESULT 13

keratin high-sulfur matrix protein IIA3 - sheep  
 N:Alternate names: M2.6 protein  
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 16-Aug-1996  
 C:Accession: A02840  
 R:Swart, L.S.; Haylett, T.  
 A:Title: Studies on the high-sulphur proteins of reduced merino wool. Amino acid se  
 A:Reference number: A90269; MOID:74022242  
 A:Accession: A02840  
 A:Molecule type: protein  
 A:Residues: 1-131 <SMA>  
 A:Experimental source: Merino wool  
 C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of othe  
 C:Superfamily: keratin high-sulfur matrix protein IIA  
 C:Keywords: duplication; hair

Query Match 19.5%; Score 65.5; DB 1; Length 131;  
 Best Local Similarity 27.6%; Pred. No. 4.6;  
 Matches 21; Conservative 5; Mismatches 19; Indels 31; Gaps 4;

11 RCVR-LHESCLGQVPCDPC-----ATCYCRFNAPC 42  
 Db 47 RCTRPICEPC--RRPVCCDPCSLQEGCCRPITCPTSCQAVVCRPCCMATTCCQPVSVQC 104

Oy 43 -YCRKLGATAMNCSR 57  
 Db 105 PCCRPTSCOPAPCSRT 120

RESULT 14

keratin high-sulfur matrix protein IIA3, major component - goat  
 N:Alternate names: M2.6 protein  
 C:Species: Capra aegagrus hircus (domestic goat)  
 C:Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 16-Aug-1996  
 C:Accession: A92978; A02840  
 R:Joubert, F.J.  
 A:Title: Studies on the high-sulphur proteins of reduced mohair. The isolation and  
 A:Reference number: A92978  
 A:Accession: A92978  
 A:Molecule type: protein  
 A:Residues: 1-132 <QOV>  
 A:Experimental source: Angora breed  
 C:Comment: Wool and hair consist of microfibrils embedded in a rigid matrix of othe  
 C:Superfamily: keratin high-sulfur matrix protein IIA  
 C:Keywords: duplication; hair

Query Match 19.5%; Score 65.5; DB 1; Length 132;  
 Best Local Similarity 27.6%; Pred. No. 4.7;  
 Matches 21; Conservative 5; Mismatches 19; Indels 31; Gaps 4;

11 RCVR-LHESCLGQVPCDPC-----ATCYCRFNAPC 42  
 Db 48 RCTRPICEPC--RRPVCCDPCSLQEGCCRPITCPTSCQAVVCRPCCMATTCCQPVSVQC 105

Oy 43 -YCRKLGATAMNCSR 57  
 Db 106 PCCRPTSCOPAPCSRT 121



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 22, 2002, 17:18:55 ; Search time 10.33 seconds

(without alignments)  
213.651 Million cell updates/sec

Title: US-09-581-894a-7

Sequence: 1 LQDREPRSSRCVRLHESCL.....FNAPCYCKLGTAMNPSRT 57

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

al number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	100.0	132	1	AGSR_HUMAN
2	298	88.7	131	1	AGSR_MOUSE
3	298	88.7	134	1	AGSR_BOVIN
4	121.5	36.2	131	1	AGSW_MOUSE
5	119	35.4	131	1	AGSW_YULYU
6	119	35.4	132	1	AGSW_HUMAN
7	116.5	34.7	133	1	AGSW_BOVIN
8	88.5	26.3	61	1	PL08_PLETR
9	84.5	25.1	46	1	PL14_PLETR
10	82.5	24.6	79	1	PL11_PLETR
11	82	24.4	45	1	PL12_PLETR
12	82	24.4	82	1	PL05_PLETR
13	70.5	20.1	3712	1	LMA_DROME
14	67.5	20.1	63	1	M84A_DROME
15	67	19.9	1587	1	LMG3_HUMAN
16	66.5	19.8	512	1	YE94_SCHRO
17	66	19.6	118	1	PA22_LATCO
18	66	19.6	1877	1	PCRS_MOUSE
19	65.5	19.5	82	1	TX32_PHONI
20	65.5	19.5	131	1	KRA3_SHEEP
21	65.5	19.5	132	1	KRA3_CAPI
22	65	19.3	123	1	PA2_TROK
23	65	19.3	247	1	ODFP_MOUSE
24	63.5	18.9	348	1	HM14_CAEEL
25	63	18.8	250	1	ODFP_HUMAN
26	62	18.5	118	1	PA24_LATSE
27	62	18.5	807	1	FSP0_RAT
28	61.5	18.3	262	1	ODFP_PIG
29	61	18.2	137	1	PA2N_VIPAA
30	61	18.2	1170	1	TSP1_HUMAN
31	61	18.2	1170	1	TSP1_MOUSE
32	60.5	18.0	262	1	ODFP_BOVIN
33	60	17.9	68	1	DISA_ECHS

#### ALIGNMENTS

RESULT	1	STANDARD	PRT	132 AA.
AC	AGSR_HUMAN	000253; 015459;		
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Agouti related protein precursor.			
GN	AGRP OR ART OR AGRT.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-97230362; PubMed-9119224;			
RA	Shutter J.R., Graham M., Kinsey A.C., Scully S., Luethy R.,			
RA	Stark K.L.;			
RT	"Hypothalamic expression of ART, a novel gene related to agouti, is			
RT	up-regulated in obese and diabetic mutant mice."			
RL	Genes Dev. 11:593-602(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-Adrenal gland;			
RX	MEDLINE-97458244; PubMed-9311920;			
RA	Oliman M.M., Wilson B.D., Yang Y.K., Kerns J.A., Chen Y., Gantz I.,			
RA	Barsh G.S.;			
RT	"Antagonism of central melanocortin receptors in vitro and in vivo by			
RT	agouti-related protein."			
RL	Science 278:135-138(1997).			
RN	[3]			
RP	DISULFIDE BONDS.			
RX	MEDLINE-98393470; PubMed-9724530;			
RA	Bures E.J., Hul J.O., Young Y., Chow D.T., Katta V., Rohde M.F.,			
RA	Zeni L., Rosenfeld R.D., Stark K.L., Hanlu M.;			
RT	Determination of disulfide structure in agouti-related protein (AGRP)			
RT	by stepwise reduction and alkylation."			
RL	Biochemistry 37:12172-12177(1998).			
RN	[4]			
RP	STRUCTURE BY NMR OF 87-132.			
RX	MEDLINE-99297561; PubMed-10371151;			
RA	Bolin K.A., Anderson D.J., Trulsson J.A., Thompson D.A., Wilken J.,			
RA	Kent S.B.H., Gantz I., Millhauser G.L.;			
RT	"NMR structure of a minimized human agouti related protein prepared by			
RT	total chemical synthesis."			
RL	FEBS Lett. 451:125-131(1999).			
CC	-1- FUNCTION: PLAYS A ROLE IN WEIGHT HOMEOSTASIS. MAY PLAY A ROLE IN			
CC	THE REGULATION OF MELANOCORTIN RECEPTORS WITHIN THE HYPOTHALAMUS			
CC	AND ADRENAL GLAND, AND THEREFORE IN THE CENTRAL CONTROL OF			
CC	FEEDING.			
CC	-1- SUBCELLULAR LOCATION: Secreted (by similarity).			
CC	-1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE ADRENAL GLAND,			
CC	SUBTHALAMIC NUCLEUS, AND HYPOTHALAMUS, WITH A LOWER LEVEL OF			
CC	EXPRESSION OCCURRING IN TESTIS, LUNG, AND KIDNEY.			
CC	-1- SIMILARITY: BELONGS TO THE AGOUTI FAMILY.			

P01058 phaseolus a  
P00612 latitanda s  
P20249 agkistrodon  
P00623 crotilus ad  
P00624 crotilus at  
O01645 drosophila  
O08707 mus musculu  
O35652 mus musculu  
P08175 drosophila  
P16343 lonchocarpu  
P20251 pseudechis  
P14615 bungarus fa



FT DISULFID 107 131 BY SIMILARITY.  
FT DISULFID 112 119 BY SIMILARITY.  
SQ SEQUENCE 134 AA; 14706 MW; F4B7AE1458B6A24B-CRC64;

Query Match 88.7%; Score 298; DB 1; Length 134;  
Best Local Similarity 87.5%; Pred. No. 5,3e-26;  
Matches 49; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 2 DQRRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCRKGIMNFCST 57  
DB 79 EKRPRSPRCVRLHESCLGQVPCDPCATCYCRFNACFCRKGIMNFCST 134

RESULT 4  
AGSM\_MOUSE STANDARD; PRT: 131 AA.

AC 003288;  
DT 01-OCT-1993 (Rel. 27, Created)  
DT 01-OCT-1993 (Rel. 27, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
Agouti switch protein precursor (Agouti signaling protein).  
ASIP OR A.

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;

SEQUENCE FROM N.A.  
RX MEDLINE=93194064; PubMed=8449404;  
RA Miller M.W., Duhl D.M., Vrieling H., Cordes S.P., Ollmann M.M.,  
Winkes B.M., Barsh G.S.;  
RT "Cloning of the mouse agouti gene predicts a secreted protein  
ubiquitously expressed in mice carrying the lethal yellow mutation."  
RL Genes Dev. 7:454-467(1993).

[2]  
SEQUENCE FROM N.A.  
RX MEDLINE=93113687; PubMed=1473152;  
RA Bultman S.J., Michaud E.J., Woychik R.P.;  
RL "Molecular characterization of the mouse agouti locus."  
Cell 71:1195-1204(1992).

-1- FUNCTION: CAUSES HAIR FOLLICLE MELANOCYTES TO SYNTHESIZE YELLOW  
PIGMENT (PHEOMELANIN) INSTEAD OF BLACK OR BROWN PIGMENT  
OTHERWISE BLACK OR BROWN BACKGROUND WHEN EXPRESSED DURING THE MID-  
PORTION OF HAIR GROWTH. IT MAY ACT AS A PHARMACOLOGICAL ANTAGONIST  
OF ALPHA-MELANOCYTE-STIMULATING HORMONE (ALPHA-MSH), BY ALTERING  
LEVELS OF INTRACELLULAR CAMP. MAY HAVE AN ANTITROPHIC ACTION ON  
MIGRATING MELANOCYTES.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: EPITHELIAL CELLS OF THE HAIR FOLLICLES AND  
THE EPIDERMIS.

-1- DEVELOPMENTAL STAGE: WIDELY EXPRESSED IN EMBRYONIC AND NEONATAL  
SKIN.

-1- SIMILARITY: BELONGS TO THE AGOUTI FAMILY.

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CC EMBL: L06451; AAA37201.1;  
DR EMBL: L06941; -; NOT\_ANNOTATED\_CDS.

DR PIR: A44330; A44330.  
DR PIR: A46298; A46298.

DR MGI: 87853; a.  
KW Signal; Glycoprotein.

FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 131 AGOUTI SWITCH PROTEIN.

FT DOMAIN 57 85 ARG/LYS-RICH (BASIC).  
FT DOMAIN 92 131 CYS-RICH.  
FT CARBOHD 39 39 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 131 AA; 14343 MW; 43544EEA32734E58 CRC64;

Query Match 36.2%; Score 121.5; DB 1; Length 131;  
Best Local Similarity 34.8%; Pred. No. 7.5e-07;  
Matches 23; Conservative 8; Mismatches 16; Indels 19; Gaps 2;

OY 3 DREPRSSRR-----CVRLHESCLGQVPCDPCATCYCRFNACFCRKGIMNFCST 47  
DB 68 EKRKSSKKKASMKRVARPPSPCVATRDSCRPAPACDPCASQCRCFPSSACTCR-- 125

OY 48 GTANMP 53  
DB 126 --VLNP 129

RESULT 5  
AGSM\_VULVU STANDARD; PRT: 131 AA.

AC P79407;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Agouti switch protein precursor (Agouti signaling protein).  
GN ASIP.

OS Vulpes vulpes (Red fox).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Vulpes.

OX NCBI\_TaxID=9627;  
RN [1]  
RP SEQUENCE FROM N.A., AND REVISIONS TO 14.

RA Vage D.I.;  
RL submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.

RN [2]  
RE SEQUENCE OF 1-125 FROM N.A.

RC TISSUE=SKIN;  
RX MEDLINE=97207656; PubMed=9054949;

RA Vage D.I., Lu D., Klungland J., Lien S., Adalsteinsson S., Cone R.D.;  
RT "A non-epistatic interaction of agouti and extension in the fox,"  
RL Vulpes vulpes."

Nat. Genet. 15:311-315(1997).

-1- SUBCELLULAR LOCATION: Secreted (by similarity).

-1- PTM: FIVE DISULFIDE BONDS ARE PRESENT (POTENTIAL).

-1- SIMILARITY: BELONGS TO THE AGOUTI FAMILY.

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CC EMBL: Y09877; CAA71004.2;

DR Signal; Glycoprotein.  
KW Signal; Glycoprotein.

FT CHAIN 1 20 POTENTIAL.  
FT SIGNAL 21 131 AGOUTI SWITCH PROTEIN.

FT DOMAIN 56 85 ARG/LYS-RICH (BASIC).  
FT DOMAIN 92 131 CYS-RICH.

FT CARBOHD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 131 AA; 14449 MW; 42185147E5B4954 CRC64;

Query Match 35.4%; Score 119; DB 1; Length 131;  
Best Local Similarity 47.6%; Pred. No. 1.4e-06;  
Matches 20; Conservative 2; Mismatches 20; Indels 0; Gaps 0;

OY 6 PRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCRKGIMNFCST 47  
DB 86 PPPRNCVATRNCSKSPAPACDPCASQCRCFPSSACTCRVL 127



```
CC -1- SIMILARITY: BELONGS TO THE AGOUTI FAMILY.
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CC -----
DR EMBL; U12775; AAB61247.1; -
DR EMBL; U12770; AAB61247.1; JOINED.
DR EMBL; U12774; AAB61247.1; JOINED.
DR EMBL; L37019; AAA89208.1; -
DR EMBL; AL035458; CAB96679.1; -
DR MIM; 600201; -.
KW Signal; Glycoprotein; Polymorphism.
FT SIGNAL; 1 22
FT CHAIN; 23 132 POTENTIAL.
FT DOMAIN; 57 86 AGOQTI SWITCH PROTEIN.
FT CATH; 93 132 ARG/LYS-RICH (BASIC).
FT CARBOHYD; 39 39 CYS-RICH.
FT VARIANT; 61 61 N-LINKED (SLC/NAC. . .) (POTENTIAL).
FT VARIAT; 61 61 0 -> P.
SO SEQUENCE 132 AA; 14515 MW; AF82CC3C747F2BB6 CRC64; /FTId=VAR_005003.

Query Match 35.4%; Score 119; DB 1; Length 132;
Best Local Similarity 50.0%; Pred. No. 1.4e-06;
Matches 22; Conservative 3; Mismatches 17; Indels 2; Gaps 1;

QY 6 FRSS--SRRCVRLHESCLGQGVPCDPACTCTCRFFNAPCYCKL 47
Db 85 PRTPLSAPCVATRNSCKPPAPACCPCASCOCRRFRSSCSCHVL 128
11: 1 11 11 11111:1 1111 : 1 1 1

RESULT 7
AGSM_BOVIN STANDARD; PRT; 133 AA.
AC Q29414;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Agouti switch protein precursor (Agouti signaling protein).
GN ASIP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Eubovae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Kidney;
RA Ouilouden A., Martin J., Rouzaud F., Petit J.M., Julien R.;
RL Submitted (FEF-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- PM: FIVE DISULFIDE BONDS ARE PRESENT (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE AGOUTI FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; X99692; CAA68004.1; -
DR EMBL; X99691; CAA68003.1; -
KW Signal; Glycoprotein.
FT SIGNAL; 1 22
FT CHAIN; 23 133 POTENTIAL.
FT CATH; 57 86 AGOQTI SWITCH PROTEIN.
FT CARBOHYD; 39 39 ARG/LYS-RICH (BASIC).
```

RT<sup>1</sup> Molecular cloning and sequencing of cDNAs encoding insecticidal peptides from the primitive hunting spider, *Plectreurys tristis*

RT<sup>1</sup> Molecular cloning and sequencing of cDNAs encoding insecticidal peptides from the primitive hunting spider, *Plectreurys tristis*

DR Pfam: PF02819; spider toxin; 1.  
KM Toxin; Neurotoxin.  
FT NON\_TER 45 45  
SQ SEQUENCE 45 AA; 4996 MW; 265ADB501AB2FAC5 CRC64;

Query Match 24.4%; Score 82; DB 1; Length 45;  
Best Local Similarity 34.1%; Pred. No. 0.0064;  
Matches 15; Conservative 5; Mismatches 22; Indels 2; Gaps 2;

OY 11 KCVRLHESCLGQVPCDCPCATCYCFRNACFCRKLGTAMNPC 54  
.: : : : : : : : : : : : : : : :  
Db 3 KCIQMGETCNG-NLPCNCEVCWCECNIMGQRCHNH-PRATREC 44

RESULT 12  
P05\_PLETR STANDARD; PRT; 82 AA.

AC P36983;  
DT 01-JUN-1994 (Rel. 29, Created)  
DI 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DD Plectoxin V/VI precursor (PLT-V and PLT-VI) (PLTVI).  
OS Plecteuys tristis (Spider).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;  
OC Araneomorphae; Haplogynae; Plecteuridae; Plecteuys.  
OX NCBI\_TaxID=33319;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-Venom gland;  
RX MEDLINE=96275925; PubMed=8763160;  
RA Leisy D.J., Mattson J.D., Quistad G.B., Kramer S.J., van Beek N.,  
RS Tsai L.W., Enderlin F.E., Woodworth A.R., Digan M.E.;  
RT "Molecular cloning and sequencing of cDNAs encoding insecticidal  
RT peptides from the primitive hunting spider, Plecteuys tristis  
RT (Simon)." ;  
RL Insect Biochem. Mol. Biol. 26:411-417(1996).  
LN [2]

RK SEQUENCE OF 34-79.  
RC TISSUE-Venom;  
RX MEDLINE=94209277; PubMed=8157635;  
RA Quistad G.B., Skinner W.S.;  
RT Hunting spider, Plecteuys tristis (Simon).";  
RL J. Biol. Chem. 269:11098-11101(1994).  
CC -1- FUNCTION: POTENT TOXIN THAT MAY PARALYZE AND/OR KILL INSECT  
CC PESTS SUCH AS H. VIRESSENS (LEPIDOPTERA), S. EXIGUA (BEET ARMYWORM)  
CC AND M. SEXTA (TOBACCO HORNMOTH).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.  
CC -1- PM: MAY POSSESS FIVE DISULFIDE BONDS.  
CC -1- PTM: PLECTOXIN V PRESUMABLY UNDERGOES POST-TRANSLATIONAL  
CC MODIFICATION TO GIVE RISE TO PLECTOXIN VI.

CC -----  
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or-send-an-email-to-licens@sib-sib.ch](http://www.isb-sib.ch/announce/or-send-an-email-to-licens@sib-sib.ch)).  
CC -----

DR EMBL; U29269; AAC47200.1; -  
DR EMBL; U29271; AAC47202.1; -  
DR EMBL; U29272; AAC47203.1; -  
DR EMBL; U29273; AAC47204.1; -  
DR EMBL; U29274; AAC47205.1; -  
DR EMBL; U29275; AAC47206.1; -  
DR EMBL; U29276; AAC47207.1; -  
DR InterPro; IPR004169; SpiderToxin.  
DR Pfam; PF02819; SpiderToxin; 1.  
KW Toxin; Neurotoxin; Signal.  
FT SIGNAL 1  
FT SIGNAL 20  
PP POTENTIAL

FT PROPER 21 33 PLECTOXIN V/VI.  
 FT CHAIN 34 79  
 FT PROPER 80 82  
 FT VARIANT 6 7  
 FT VARIANT 11 11 PS-> I (IN CLONES PSCI267, PSCI268, PSCI270 AND PSCI272).  
 FT VARIANT 19 19 V-> I (IN CLONES PSCI268, PSCI270 AND PSCI272).  
 FT VARIANT 19 19 F-> S (IN CLONES PSCI268, PSCI270 AND PSCI272).  
 SO SEQUENCE 82 AA: 9241 MM: F74A45703BC77965 CRC64;

Query Match 24.4%; Score 82; DB 1; Length 82;  
 Best Local Similarity 34.1%; Pred. No. 0.01;  
 Matches 15; Conservative 5; Mismatches 22; Indels 2; Gaps 2;

QY 11 RCVRHESGICQGVPCPCATCTCFRNFATCYCKRLGTAMPC 54  
 36 KCIQWETCTCG-NLPCQNECVACCECINGOMCRNH-PRATWEC 77

ID LMA\_DROME STANDARD: PRT; 3712 AA.  
 AC 000174;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Laminin alpha chain precursor.  
 GN LANA OR LAMA.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93049203; PubMed=1425586;  
 RA Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,  
 RA Fessler J.H.;  
 RT "Laminin A chain: expression during Drosophila development and  
 RT genomic sequence."  
 RL EMBO J. 11:4519-4527(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94038678; PubMed=8223265;  
 RA Henchcliffe C., Garcia-Alonso L., Tang J., Goodman C.S.;  
 RA "Genetic analysis of laminin A reveals diverse functions during  
 RA morphogenesis in Drosophila."  
 RL Development 118:325-337(1993).  
 RN [3]  
 RP SEQUENCE OF 1762-3712 FROM N.A.  
 RX MEDLINE=92078147; PubMed=1744083;  
 RA Garrison K., Mackrell A.J., Fessler J.H.;  
 RA "Drosophila laminin A chain sequence, interspecies comparison, and  
 RA domain structure of a major carboxyl portion."  
 RL J. Biol. Chem. 266:22899-22904(1991).  
 CC -1- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR. LAMININ  
 CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF  
 CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING  
 CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.  
 CC -1- FUNCTION: DIVERSE FUNCTIONS DURING MORPHOGENESIS IN DROSOPHILA.  
 CC COMPLETE LOSS-OF-FUNCTION MUTATIONS LEAD TO LATE EMBRYONIC  
 CC LETHALITY. CERTAIN PARTIAL LOSS-OF-FUNCTION MUTATIONS GIVE RAISE  
 CC TO ESCAPER ADULTS, WHICH HAVE ROUGH EYES ASSOCIATED WITH CHANGES  
 CC IN CELL FATE AND PATTERN, MISSHAPEN LEGS AND DEFECTS IN WING  
 CC STRUCTURE.  
 CC -1- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE  
 CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND  
 CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE  
 CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.  
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT

CC MEMBRANES (MAJOR COMPONENT).  
 CC -1- TISSUE SPECIFICITY: NEWLY FORMED MESODERM AND LATER PROMINENTLY  
 CC EXPRESSED IN HEMOCYTES, WHICH ALSO SYNTHESIZE COLLAGEN IV.  
 CC -1- DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO  
 CC DEVELOPMENT AT 10-12 HOURS.  
 CC -1- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT  
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.  
 CC -1- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.  
 CC -1- SIMILARITY: CONTRAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).  
 CC -1- SIMILARITY: CONTRAINS 21.5 LAMININ EGF-LIKE DOMAINS.  
 CC -1- SIMILARITY: CONTRAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT  
 CC SIMILAR TO LAMININ DOMAIN IV).  
 CC -1- SIMILARITY: CONTRAINS 5 LAMININ G-LIKE DOMAINS.  
 CC -----  
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 CC or send an email to [license@sdb.ch](mailto:license@sdb.ch)).  
 CC -----  
 CC EMBL: M96388; AAA28662.1; -  
 CC EMBL: L07288; AAC37178.1; -  
 CC EMBL: M75882; AAA28661.1; -  
 CC HSSP: P02468; ITRF.  
 CC FlyBase: FBgn002526; LANA.  
 CC InterPro: IPR000561; EGF-like.  
 CC InterPro: IPR001886; LAMNT.  
 CC InterPro: IPR000034; Laminin\_B.  
 CC InterPro: IPR002049; Laminin\_EGF.  
 CC InterPro: IPR001791; Laminin\_G.  
 CC InterPro: IPR001330; Prenyltn.  
 CC Pfam: PF00053; Laminin\_B; 1.  
 CC Pfam: PF00052; Laminin\_EGF; 20.  
 CC Pfam: PF00054; Laminin\_G; 5.  
 CC Pfam: PF00055; Laminin\_Nterm; 1.  
 CC PRINTS: PR00011; EGF\_LAMININ.  
 CC ProDom: PD002082; LAMNT; 1.  
 CC ProDom: PD003031; Laminin\_B; 1.  
 CC SMART: SM00180; EGF\_Lam; 17.  
 CC SMART: SM00001; EGF\_Like; 1.  
 CC SMART: SM00281; Lamb; 1.  
 CC SMART: SM00282; Lamb; 5.  
 CC SMART: SM00136; LAMNT; 1.  
 CC PROSITE: PS00022; EGF\_1; 17.  
 CC PROSITE: PS01186; EGF\_2; 5.  
 CC PROSITE: PS01248; LAMININ\_TYPE\_EGF; 19.  
 CC PROSITE: PS00025; LAM\_G\_DOMAIN; 5.  
 CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;  
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.  
 CC POTENTIAL.  
 CC LAMININ ALPHA CHAIN.  
 CC LAMININ N-TERMINAL (DOMAIN VI).  
 CC LAMININ EGF-LIKE 1.  
 CC LAMININ EGF-LIKE 2.  
 CC LAMININ EGF-LIKE 3.  
 CC LAMININ EGF-LIKE 4.  
 CC LAMININ EGF-LIKE 5.  
 CC LAMININ EGF-LIKE 6.  
 CC LAMININ EGF-LIKE 7.  
 CC LAMININ EGF-LIKE 8.  
 CC LAMININ EGF-LIKE 9.  
 CC LAMININ EGF-LIKE 10.  
 CC LAMININ EGF-LIKE 11 (INCOMPLETE).  
 CC DOMAIN IV'.  
 CC LAMININ EGF-LIKE 12.  
 CC LAMININ EGF-LIKE 13.  
 CC LAMININ EGF-LIKE 14.  
 CC LAMININ EGF-LIKE 15.  
 CC LAMININ EGF-LIKE 16 (N-TERMINAL).  
 CC LAMININ DOMAIN IV (DOMAIN IV).  
 CC LAMININ EGF-LIKE 16 (C-TERMINAL).

FT DOMAIN 1809 1858 LAMININ EGF-LIKE 17.  
 FT DOMAIN 1859 1916 LAMININ EGF-LIKE 18.  
 FT DOMAIN 1917 1969 LAMININ EGF-LIKE 19.  
 FT DOMAIN 1970 2016 LAMININ EGF-LIKE 20.  
 FT DOMAIN 2017 2063 LAMININ EGF-LIKE 21.  
 FT DOMAIN 2064 2111 LAMININ EGF-LIKE 22.  
 FT DOMAIN 2112 2671 LAMININ II AND I.  
 FT DOMAIN 2672 2868 LAMININ G-LIKE 1.  
 FT DOMAIN 2876 3048 LAMININ G-LIKE 2.  
 FT DOMAIN 3055 3223 LAMININ G-LIKE 3.  
 FT DOMAIN 3349 3528 LAMININ G-LIKE 4.  
 FT DOMAIN 3534 3709 LAMININ G-LIKE 5.  
 FT DOMAIN 2178 2249 COILED COIL (POTENTIAL).  
 FT DOMAIN 2301 2321 COILED COIL (POTENTIAL).  
 FT DOMAIN 2376 2450 COILED COIL (POTENTIAL).  
 FT DOMAIN 2541 2676 COILED COIL (POTENTIAL).  
 FT DOMAIN 3270 3296 POLY-THR.  
 FT DISULFID 273 282 BY SIMILARITY.  
 FT DISULFID 275 296 BY SIMILARITY.  
 FT DISULFID 298 307 BY SIMILARITY.  
 FT DISULFID 310 330 BY SIMILARITY.  
 FT DISULFID 333 342 BY SIMILARITY.  
 FT DISULFID 335 367 BY SIMILARITY.  
 FT DISULFID 370 379 BY SIMILARITY.  
 FT DISULFID 382 400 BY SIMILARITY.  
 FT DISULFID 403 414 BY SIMILARITY.  
 FT DISULFID 405 421 BY SIMILARITY.  
 FT DISULFID 423 432 BY SIMILARITY.  
 FT DISULFID 435 445 BY SIMILARITY.  
 FT DISULFID 448 460 BY SIMILARITY.  
 FT DISULFID 450 468 BY SIMILARITY.  
 FT DISULFID 470 479 BY SIMILARITY.  
 FT DISULFID 482 492 BY SIMILARITY.  
 FT DISULFID 495 507 BY SIMILARITY.  
 FT DISULFID 497 514 BY SIMILARITY.  
 FT DISULFID 516 525 BY SIMILARITY.  
 FT DISULFID 528 538 BY SIMILARITY.  
 FT DISULFID 541 553 BY SIMILARITY.  
 FT DISULFID 543 560 BY SIMILARITY.  
 FT DISULFID 562 571 BY SIMILARITY.  
 FT DISULFID 574 584 BY SIMILARITY.  
 FT DISULFID 587 599 BY SIMILARITY.  
 FT DISULFID 589 605 BY SIMILARITY.  
 FT DISULFID 607 616 BY SIMILARITY.  
 FT DISULFID 619 629 BY SIMILARITY.  
 FT DISULFID 632 644 BY SIMILARITY.  
 FT DISULFID 634 650 BY SIMILARITY.  
 FT DISULFID 652 661 BY SIMILARITY.  
 FT DISULFID 664 674 BY SIMILARITY.  
 FT DISULFID 677 691 BY SIMILARITY.  
 FT DISULFID 679 700 BY SIMILARITY.  
 FT DISULFID 702 711 BY SIMILARITY.  
 FT DISULFID 714 729 BY SIMILARITY.  
 FT DISULFID 732 746 BY SIMILARITY.  
 FT DISULFID 734 753 BY SIMILARITY.  
 FT DISULFID 755 764 BY SIMILARITY.  
 FT DISULFID 767 782 BY SIMILARITY.  
 FT DISULFID 1375 1387 BY SIMILARITY.  
 FT DISULFID 1377 1394 BY SIMILARITY.  
 FT DISULFID 1396 1405 BY SIMILARITY.  
 FT DISULFID 1408 1418 BY SIMILARITY.  
 FT DISULFID 1421 1429 BY SIMILARITY.  
 FT DISULFID 1423 1436 BY SIMILARITY.  
 FT DISULFID 1438 1447 BY SIMILARITY.  
 FT DISULFID 1450 1463 BY SIMILARITY.  
 FT DISULFID 1466 1480 BY SIMILARITY.  
 FT DISULFID 1468 1487 BY SIMILARITY.  
 FT DISULFID 1489 1498 BY SIMILARITY.  
 FT DISULFID 1501 1511 BY SIMILARITY.  
 FT DISULFID 1514 1526 BY SIMILARITY.  
 FT DISULFID 1516 1533 BY SIMILARITY.  
 FT DISULFID 1535 1544 BY SIMILARITY.  
 FT DISULFID 1547 1562 BY SIMILARITY.

FT DISULFID 1859 1874 BY SIMILARITY.  
 FT DISULFID 1861 1885 BY SIMILARITY.  
 FT DISULFID 1887 1896 BY SIMILARITY.  
 FT DISULFID 1899 1914 BY SIMILARITY.

Query Match 21.0% Score 70.5; DB 1; Length 3712;  
 Best Local Similarity 37.0%; Pred. No. 3.4;  
 Matches 17; Conservative 3; Mismatches 17; Indels 9; Gaps 2;

QY 21 GQVPC-----CDPCATCYCFEFA-FCYCRIGTANPCSR 57  
 DB 465 GQPCRCRNFAGACVCKCABEYTGPEPCCKACECKISITDCNVT 510

RESULT 14  
 M84A\_DROME STANDARD; PRT; 63 AA.  
 AC 001642: 09VIA3:  
 DT 01-JUL-1993 (Rel. 26, Last Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Male specific sperm protein Mst84da.  
 GN Mst84da OR CG17946.  
 OS Drosophila melanogaster (Fruit fly)  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OREGON-R;  
 RA MEDLINE=92102953; PubMed=1684716;  
 RA Kuhn R., Kuhn C., Boersch D., Glaetzer K.H., Schaefer U.,  
 RA Schaefer M.;  
 RT "A cluster of four genes selectively expressed in the male germ line  
 RT of Drosophila melanogaster.";  
 RL Mech. Dev. 35:143-151(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BERKELEY;  
 RA MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George K.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,  
 RA Folsler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacle J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheefer F., Shen H.,  
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venner E., Wang A.H., Wang X.,  
 RA Wang Z.-T., Wassarman D.A., Weinstein G.M., Weissendach J.,

DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

Best Local Similarity 26.7%; Pred. NO. 4.2;  
Matches 20; Conservative 10; Mismatches 17; Indels 1

Query Match	19.98;	Score 67;	DB 1;	Length 1587;
Best Local Similarity	26.78;	Pred. No. 4.2;		
Matches	20;	Conservative	10;	Mismatches 17;
				Indels 28;
				Gaps 5;

**Tue Jul 23 09:23:53 2002**

us-09-581-894a-7.rsp

Page 10

[illegible]

Search completed: July 22, 2002, 17:22:27  
Job time: 212 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 22, 2002, 17:18:35 ; Search time 25.56 Seconds  
(without alignments)  
385.787 Million cell updates/sec

Title: US-09-581-894A-7  
Perfect score: 336  
Sequence: 1 LODREPRSRRCVRLHESCL.....FNACFCYCRKLTATMPCSR 57

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	87.5	121	6	09GLM5
2	294	87.5	134	6	09TUI8
3	240	71.4	71	13	090VY7
4	240	71.4	154	13	09PWG2
5	240	71.4	165	13	09WTR0
6	212.5	63.2	78	11	09OKJ3
7	124.5	37.1	131	6	09MTU1
8	120.5	35.9	133	6	095MP2
9	116.5	34.7	131	11	093VA2
10	73.5	21.9	606	13	098UF9
11	72.5	21.6	161	12	066216
12	72.5	21.6	203	12	066236
13	70.5	21.0	3712	5	09VRW0
14	69.5	20.7	138	13	091968
15	69.5	20.7	498	10	094816
16	69	20.5	808	5	09V995

17	68	20.2	1486	4	014637	014637 homo sapien
18	65.5	19.5	82	5	076201	076201 phonentria
19	65	19.3	114	5	095529	095529 drosophila
20	65	19.3	1137	4	09H8C1	09H8C1 homo sapien
21	65	19.3	1918	4	09BQM7	09BQM7 homo sapien
22	65	19.3	1925	4	09P2E3	09P2E3 homo sapien
23	64.5	19.2	104	10	094IH5	094IH5 vigma mungo
24	64.5	19.2	627	4	09H7R0	09H7R0 homo sapien
25	63.5	18.9	280	4	09P100	09P100 homo sapien
26	63.5	18.9	280	4	09BAV2	09BAV2 homo sapien
27	63.5	18.9	289	11	09R059	09R059 mus musculu
28	63.5	18.9	351	5	09NBV6	09NBV6 strongyloce
29	62.5	18.6	1075	5	09NC90	09NC90 strongyloce
30	62.5	18.6	3767	5	09UA13	09UA13 caenorhabdi
31	62	18.5	624	4	094862	094862 homo sapien
32	62	18.5	1056	4	09H3R0	09H3R0 homo sapien
33	62	18.5	1100	4	094877	094877 homo sapien
34	62	18.5	1487	10	09MA08	09MA08 arabidopsis
35	61.5	18.3	411	11	09JUR6	09JUR6 mus musculu
36	61.5	18.3	558	4	096E63	096E63 homo sapien
37	61.5	18.3	792	13	090X43	090X43 gallus gall
38	61.5	18.3	1095	13	090XG4	090XG4 gallus gall
39	61.5	18.3	1119	5	018034	018034 caenorhabdi
40	61	18.2	137	13	091967	091967 vipera ammo
41	61	18.2	151	5	017508	017508 caenorhabdi
42	61	18.2	376	4	015667	015667 homo sapien
43	61	18.2	807	4	09HC86	09HC86 homo sapien
44	61	18.2	2104	5	021281	021281 caenorhabdi
45	61	18.2	2104	5	0964N4	0964N4 caenorhabdi

## ALIGNMENTS

RESULT 1  
ID 09GLM5 PRELIMINARY; PRT; 121 AA.  
AC 09GLM5:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE ACODIT-RELATED PROTEIN (FRAGMENT).  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9623;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HYPOPHALMUS;  
RA Mattern R.L., Dyer C.J.;  
RT "Effects of weaning and piglet size on neuroendocrine regulators of  
RT feed intake in pigs."  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF220531; AAC09464.1;  
FT NON TER 1  
SQ SEQUENCE 121 AA; 13276 MW; DD736F01B5B5766E CRC64;

Query Match 87.5%; Score 294; DB 6; Length 121;  
Best Local Similarity 87.5%; Pred. No. 2e-33;  
Matches 49; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 LODREPRSRRCVRLHESCLGQVPCDCPCATCYCFNACFCYCRKLTATMPCSR 57  
Db 66 EGRARSRRCVRLHESCLGQVPCDCPCATCYCFNACFCYCRKLTATMPCSR 121

RESULT 2  
ID 09TUI8 PRELIMINARY; PRT; 134 AA.  
AC 09TUI8:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)



RESULT	6			
090XJ3				
ID	090XJ3	PRELIMINARY;	PRT;	78 AA.
AC	090XJ3;			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	AGOUTI RELATED PROTEIN (FRAGMENT).			
GN	AGRP.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus			
NCBI_TaxId=10116;				
GN	[1]			

RESULT	10
098UF9	
ID	098UF9
AC	098UF9;
DT	01-JUN-2001 (TREMblrel. 17, created)
DT	01-JUN-2001 (TREMblrel. 17, last sequence update)
DT	01-DEC-2001 (TREMblrel. 19, last annotation update)
DE	HEMORRHAGIC METALLOPROTEINASE HP3.
DE	Bothrops jararaca (Jararaca).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC	Viperidae; Crotalinae; Bothrops.
OX	NCBI_TaxID=8724;
RN	[1]
RP	SEQUENCE FROM N.A.

RC TISSUE-VENOM GLAND;  
 RA Silva C.A., Mentele R., Fink E., Camargo A.C.M., Serrano S.M.T.;  
 RT "Molecular cloning of H33, an hemorrhagic metalloproteinase from the  
 RL venom of Bothrops jararaca.";  
 CC Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.  
 DR -1- SIMILARITY: BELONGS TO THE DISINTEGRIN FAMILY.  
 DR EMBL: AF149788; AAC48931.3; -  
 DR HSSP: P18619; 1FVL.  
 DR InterPro: IPR001762; Disintegrin.  
 DR InterPro: IPR002870; Pep\_M12B-Propep.  
 DR InterPro: IPR001590; Reprolysin.  
 DR InterPro: IPR000130; Zn\_Metpeptidase.  
 DR Pfam: PF00200; disintegrin.1.  
 DR Pfam: PF01562; Pep\_M12B-propep.1.  
 DR PRINTS: PR00289; Reprolysin.1.  
 DR PRODOM: PD000664; Disintegrin.1.  
 DR SMART: SM00050; DISIN.1.  
 DR PROSITE: PS50215; ADAM\_MERO.1.  
 DR PROSITE: PS00427; DISINTEGRIN.1.  
 DR PROSITE: PS50214; DISINTEGRIN.2.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 SO SEQUENCE 606 AA; 68044 MW; 3E57A0A76B61D0E CRC64;

Query Match 21.9%; Score 73.5; DB 13; Length 606;  
 Best Local Similarity 24.0%; Pred. No. 0.041; Mismatches 23; Indels 41; Gaps 4;  
 Matches 23; Conservative 9;

OY 2 QDREPRSSRCVRLHESCLGQGVPC-----CDPCA-----TCYCRF 37  
 DB 457 QDREPRSSRCVRLHESCLGQGVPC-----CDPCA-----TCYCRF 37  
 OY 38 -----FN-----AFCYCRKLTGRANMPCSR 56  
 DB 517 GSNATVAEDGCEFNENGDKRYFCRQSGVNNPCAQ 552

RESULT 11  
 ID 066216 PRELIMINARY; PRT; 161 AA.  
 AC 066216;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CYSTEINE-RICH PROTEIN (FRAGMENT).  
 OS Campoletis sonorensis virus (CSV).  
 OS Viruses; dsDNA viruses, no RNA stage; Polydnaviridae; Ichnovirus.  
 NCBI\_TaxID=10484;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-87321096; PubMed-3629971;  
 RA Blissard G.W., Smith O.P., Summers M.D.;  
 RT "Two related viral genes are located on a single superhelical DNA  
 RL segment of the multipartite Campoletis sonorensis virus genome.";  
 RL Virology 160:120-134(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-93234578; PubMed-8475127;  
 RA Dill-Hall S.D., Webb B.A., Summers M.D.;  
 RT "Structure and evolutionary implications of a 'cysteine-rich',  
 RL Campoletis sonorensis polydnavirus gene family.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:3765-3769(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Cui L., Webb B.A.;  
 RT "Promoter analysis of a cysteine-rich Campoletis sonorensis  
 RL polydnavirus gene.";  
 RL J. Gen. Virol. 0:0-0(1997).  
 DR EMBL: L08245; AAB60899.1; -  
 DR InterPro: IPR001211; PLP\_A2.  
 DR PROSITE: PS00118; PA2\_HIS; UNKNOWN\_1.  
 FT NON\_TER 161 161

SO SEQUENCE 161 AA; 17576 MW; F7D52DF0ABBA1114 CRC64;

Query Match 21.6%; Score 72.5; DB 12; Length 161;  
 Best Local Similarity 33.3%; Pred. No. 0.017; Mismatches 14; Indels 1; Gaps 1;  
 Matches 14; Conservative 7;

OY 1 LQDREPRSSRCVRLHESCLGQGVPCDPCATCYCRFFNAFC 42  
 DB 121 VDDPAKPEPTCMANWDYCLGFGKPCDDHSICF-KFEGGIC 161

RESULT 12  
 ID 066236 PRELIMINARY; PRT; 203 AA.  
 AC 066236;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE HYPOTHETICAL 22.7 KDA PROTEIN.  
 GN WHV1.0.  
 OS Campoletis sonorensis virus (CSV).  
 OS Viruses; dsDNA viruses, no RNA stage; Polydnaviridae; Ichnovirus.  
 NCBI\_TaxID=10484;  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-87321096; PubMed-3629971;  
 RA Blissard G.W., Smith O.P., Summers M.D.;  
 RT "Two related viral genes are located on a single superhelical DNA  
 RL segment of the multipartite Campoletis sonorensis virus genome.";  
 RL Virology 160:120-134(1987).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-98001373; PubMed-9343208;  
 RA Cui L., Webb B.A.;  
 RT "Homologous sequences in the Campoletis sonorensis polydnavirus genome  
 RT are implicated in replication and nesting of the W segment family.";  
 RL J. Virol. 71:8504-8513(1997).  
 DR EMBL: M17405; AAB6405.1; -  
 DR EMBL: AF004378; AAC58527.1; -  
 DR InterPro: IPR001211; PLP\_A2.  
 DR PROSITE: PS00118; PA2\_HIS; UNKNOWN\_1.  
 KM Hypothetical protein.  
 SO SEQUENCE 203 AA; 22659 MW; A2295456A1440404 CRC64;

Query Match 21.6%; Score 72.5; DB 12; Length 203;  
 Best Local Similarity 33.3%; Pred. No. 0.021; Mismatches 20; Indels 1; Gaps 1;  
 Matches 14; Conservative 7;

OY 1 LQDREPRSSRCVRLHESCLGQGVPCDPCATCYCRFFNAFC 42  
 DB 121 VDDPAKPEPTCMANWDYCLGFGKPCDDHSICF-KFEGGIC 161

RESULT 13  
 ID 09VRM0 PRELIMINARY; PRT; 3712 AA.  
 AC 09VRM0;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE LANA PROTEIN.  
 GN LANA OR CG10236.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;

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Query Match          21.0%; Score 70.5; DB 5; Length 3712;
Best Local Similarity 37.0%; Pred. No. 0.54;
Matches 17; Conservative 3; Mismatches 17; Indels 9; Gaps 2;

QY 21 GQOVPC-----CDPCATCCYCFEFNA-FCYCRILGTAMNCSRT 57
    ||| || | | | | | | | | | | | | | | | | | | |
Db 465 GQCCCKRINFAGATYCKQCAEGTYGPFPECKRACCKNKIGSTTNCCNVF 510

RESULT 14
ID 091968 PRELIMINARY; PRT; 138 AA.
AC 091968;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PHOSPHOLIPASE A2 PRECURSOR (EC 3.1.1.4).
OS Trimeresurus mucrosquamatus (Taiwan habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Chelonia; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Protobothrops.
OX NCBI_TaxID=103944;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SNAKE VENOM GLAND;
RA Tsai I.;
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; X77646; CAB88411.1; -.
DR HSSP; P51972; IVAP.
DR InterPro; IPR001211; PLP_A2.
DR Pfam; PF00068; Phoslip; 1.
DR PRINTS; PR00389; PPHPLIPASEA2.
DR ProDom; PD000303; PLP_A2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KM Signal; Hydrolase.
FT SIGNAL 1
FT CHAIN 17 138 POTENTIAL.
FT FT PHOSPHOLIPASE A2.
SQ SEQUENCE 138 AA; 15739 MM; BRCBD597BF9A366C CRC64;

Query Match          20.7%; Score 69.5; DB 13; Length 136;
Best Local Similarity 27.9%; Pred. No. 0.04;
Matches 19; Conservative 7; Mismatches 19; Indels 23; Gaps 4;

QY 5 EPR-SSRRCVNLHESCLGQVPC-----C--DPC--ATCYCFEFNAF 41
    ||| || | | | | | | | | | | | | | | | | | | |
Db 51 EPRKDTDCGCVHDCYGLTACSPKLDMTYYSQKNEDIVCGGDDPCRKKEICDCKAAAI 110

QY 42 CYCRILGT 49
    | : |||
Db 111 CFLNLTGT 118

RESULT 15
ID 094816 PRELIMINARY; PRT; 498 AA.
AC 094816;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHEICAL 54.3 KDA PROTEIN.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RA Spiegel L.; Nascimento L.; de la Bastide M.; Preston R.; Kirchoff K.;

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RA King L., Baker J., Vill M.D., Zutavern T., Santos L., Kult K.,  
 RA Cunniff D.M., Miller B., Bell M., Balija V., Shah R., Bahret A.,  
 RA Yang C., O'Shaughnessy A., Palmer L., Dedhia N., McCombie W.R.,  
 RT "Genomic Sequence for Oryza sativa, Nipponbare strain, clone  
 RT OSJNBa0060a14, from chromosome 10, complete sequence."  
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AC021893; AAK98676.1;  
 KW Hypothetical protein.  
 SQ SEQUENCE 498 AA; 54325 MW; 909432BDE466AA76 CRC64;

Query Match 20.7%; Score 69.5; DB 10; Length 498;  
 Best Local Similarity 26.6%; Pred. No. 0.12;  
 Matches 21; Conservative 3; Mismatches 24; Indels 31; Gaps 2;

OY 1 LQDERPSSRRCYRLHESCLGQGVPC-----DPCATC----- 33  
 DB 357 LSKSPMGSRRIYVGTGDLVAGVLPCCYVHAECLEERTTPKGOKHDPACDRLSGKDT 416  
 34 ----YCRFFNAFCYCRKLG 48  
 417 EQMSICRLRNGFPRLRSLG 435

Search completed: July 22, 2002, 17:22:11  
 Job time: 216 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 22, 2002, 17:13:20 ; Search time 12.91 Seconds  
(without alignments)  
107.843 Million cell updates/sec

Title: US-09-581-894A-7

Perfect score: 336  
Sequence: 1 LODREPRSSRCVRLHESCL.....FNATCYCKRLGTAMPCSRRT 57

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/PTCUTS.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	100.0	132	1	US-08-757-541-7
2	336	100.0	132	1	US-08-757-541-11
3	336	100.0	132	3	US-09-033-275-7
4	336	100.0	132	3	US-09-033-275-11
5	336	100.0	132	4	US-09-342-581-7
6	336	100.0	132	4	US-09-342-581-11
7	321	95.5	54	1	US-08-757-541-8
8	321	95.5	54	3	US-09-033-275-8
9	321	95.5	54	4	US-09-342-581-8
10	299	89.0	50	4	US-09-031-902-2
11	298	88.7	131	1	US-08-757-541-10
12	298	88.7	131	3	US-09-033-275-10
13	298	88.7	131	4	US-09-342-581-10
14	286	85.1	48	4	US-09-240-078-1
15	181	53.9	32	4	US-09-240-078-2
16	180	53.6	32	4	US-09-240-078-8
17	162	48.2	32	4	US-09-240-078-9
18	159	47.3	32	4	US-09-240-078-3
19	159	47.3	32	4	US-09-240-078-4
20	159	47.3	32	4	US-09-240-078-5
21	158	47.0	32	4	US-09-240-078-11
22	126.5	37.6	32	4	US-09-240-078-10
23	121.5	36.2	131	3	US-09-102-977-2
24	121.5	36.2	131	4	US-09-034-088A-2
25	119	35.4	22	4	US-09-240-078-19
26	119	35.4	132	4	US-09-034-088A-4
27	113	33.6	22	4	US-09-240-078-12

28	113	33.6	22	4	US-09-240-078-21	Sequence 21, Appl
29	111	33.0	22	4	US-09-240-078-20	Sequence 20, Appl
30	111	33.0	22	4	US-09-240-078-22	Sequence 22, Appl
31	111	33.0	22	4	US-09-240-078-23	Sequence 23, Appl
32	101	30.1	20	4	US-09-240-078-24	Sequence 24, Appl
33	91	27.1	61	1	US-08-221-285-35	Sequence 35, Appl
34	91	27.1	61	4	US-08-428-596A-10	Sequence 10, Appl
35	84.5	25.1	46	1	US-08-221-285-6	Sequence 6, Appl
36	84.5	25.1	46	1	US-08-428-596A-10	Sequence 10, Appl
37	84.5	25.1	46	4	US-08-428-596A-6	Sequence 6, Appl
38	84.5	25.1	46	4	US-08-428-596A-10	Sequence 10, Appl
39	83	24.7	32	4	US-09-240-078-13	Sequence 13, Appl
40	82.5	24.6	46	1	US-08-221-285-7	Sequence 7, Appl
41	82.5	24.6	46	4	US-08-428-596A-7	Sequence 7, Appl
42	82	24.4	45	1	US-08-221-285-8	Sequence 8, Appl
43	82	24.4	45	4	US-08-428-596A-8	Sequence 8, Appl
44	82	24.4	46	1	US-08-221-285-5	Sequence 5, Appl
45	82	24.4	46	4	US-08-428-596A-5	Sequence 5, Appl

#### ALIGNMENTS

RESULT 1  
US-08-757-541-7  
Sequence 7, Application US/08757541

Patent No. 576877  
GENERAL INFORMATION:

APPLICANT: Stark, Kevin Lee

APPLICANT: Luethy, Roland

TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESSES:

ADDRESSEE: AMGEN INC.

STREET: 1840 DEHAVILLAND DRIVE

CITY: THOUSAND OAKS

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757,541

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: OLESKI, NANCY A

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-402A

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-757-541-7

Query Match

Best Local Similarity 100.0%; Score 336; DB 1; Length 132;

Pred. No. 2.3e-28;

Matches 57; Conservative 0; Mismatches 0; Indels 0;

Gaps 0;

DB 76 LODREPRSSRCVRLHESCLGQVPCDPCATCYCFNATCYCKRLGTAMPCSRRT 132

RESULT 2

US-08-757-541-11

Sequence 11, Application US/08757541  
Patent No. 5766877  
GENERAL INFORMATION:  
APPLICANT: Stark, Kevin Lee  
APPLICANT: Luethy, Roland  
TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,541  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: OLESKI, NANCY A  
REGISTRATION NUMBER: 34,688  
REFERENCE/DOCKET NUMBER: A-402A  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-757-541-11

Query Match 100.0%; Score 336; DB 1; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDREPRSSRCVRLHESCLGQVPCPCATCYCRFFNACFCYCKRLGTANMPCSR 57  
Db 76 LQDREPRSSRCVRLHESCLGQVPCPCATCYCRFFNACFCYCKRLGTANMPCSR 132

RESULT 3  
Sequence 7, Application US/09033275  
Patent No. 6060589  
GENERAL INFORMATION:  
APPLICANT: Stark, Kevin Lee  
APPLICANT: Luethy, Roland  
TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/033,275  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,541

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: OLESKI, NANCY A  
REGISTRATION NUMBER: 34,688  
REFERENCE/DOCKET NUMBER: A-402A  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 132 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-033-275-7

Query Match 100.0%; Score 336; DB 3; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQDREPRSSRCVRLHESCLGQVPCPCATCYCRFFNACFCYCKRLGTANMPCSR 57  
Db 76 LQDREPRSSRCVRLHESCLGQVPCPCATCYCRFFNACFCYCKRLGTANMPCSR 132

RESULT 4  
Sequence 11, Application US/09033275  
Patent No. 6060589  
GENERAL INFORMATION:  
APPLICANT: Stark, Kevin Lee  
APPLICANT: Luethy, Roland  
TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: AMGEN INC.  
STREET: 1840 DEHAVILLAND DRIVE  
CITY: THOUSAND OAKS  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/033,275  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/757,541

RESULT 5  
US-09-342-581-7  
; Sequence 7, Application US/09342581  
; Patent No. 6203995  
; GENERAL INFORMATION:  
; APPLICANT: Stark, Kevin Lee  
; APPLICANT: Luethy, Roland  
; TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: AMGEN INC.  
; STREET: 1840 DEHAVILLAND DRIVE  
; CITY: THOUSAND OAKS  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/342,581  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/033,275  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLESKI, NANCY A  
; REGISTRATION NUMBER: 34,688  
; REFERENCE/DOCKET NUMBER: A-402A  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-342-581-7

Query Match 100.0%; Score 336; DB 4; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 LODREPRSSRCVRLHESCLGQGVPCCDPCATCYCFNFNAFCYCRKLTAMNPCSRT 57  
|||||  
76 LODREPRSSRCVRLHESCLGQGVPCCDPCATCYCFNFNAFCYCRKLTAMNPCSRT 132

RESULT 6  
US-09-342-581-11  
; Sequence 11, Application US/09342581  
; Patent No. 6203995  
; GENERAL INFORMATION:  
; APPLICANT: Stark, Kevin Lee  
; APPLICANT: Luethy, Roland  
; TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: AMGEN INC.  
; STREET: 1840 DEHAVILLAND DRIVE  
; CITY: THOUSAND OAKS  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/342,581  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/033,275  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLESKI, NANCY A  
; REGISTRATION NUMBER: 34,688  
; REFERENCE/DOCKET NUMBER: A-402A  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 132 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-09-342-581-11

Query Match 100.0%; Score 336; DB 4; Length 132;  
Best Local Similarity 100.0%; Pred. No. 2.3e-28;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LODREPRSSRCVRLHESCLGQGVPCCDPCATCYCFNFNAFCYCRKLTAMNPCSRT 57  
Db 76 LODREPRSSRCVRLHESCLGQGVPCCDPCATCYCFNFNAFCYCRKLTAMNPCSRT 132

RESULT 7  
US-08-757-541-8  
; Sequence 8, Application US/08757541  
; Patent No. 5766877  
; GENERAL INFORMATION:  
; APPLICANT: Stark, Kevin Lee  
; APPLICANT: Luethy, Roland  
; TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: AMGEN INC.  
; STREET: 1840 DEHAVILLAND DRIVE  
; CITY: THOUSAND OAKS  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 91320-1789  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,541  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: OLESKI, NANCY A  
; REGISTRATION NUMBER: 34,688  
; REFERENCE/DOCKET NUMBER: A-402A  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 54 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-757-541-8

Query Match 95.5%; Score 321; DB 1; Length 54;  
Best Local Similarity 100.0%; Pred. No. 3.8e-27;  
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 4 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 57  
DB 1 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 54

## RESULT 8

US-09-033-275-8

Sequence 8, Application US/09033275

Patent No. 6060589

GENERAL INFORMATION:

APPLICANT: Stark, Kevin Lee

APPLICANT: Laethy, Roland

TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: 1840 DEHAVILLAND DRIVE

CITY: THOUSAND OAKS

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/033,275

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/757,541

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OLESKI, NANCY A

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-402A

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-033-275-8

Query Match 95.5%; Score 321; DB 3; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.8e-27;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 57  
DB 1 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 54

## RESULT 9

US-09-342-581-8

Sequence 8, Application US/09342581

Patent No. 6203995

GENERAL INFORMATION:

APPLICANT: Stark, Kevin Lee

APPLICANT: Laethy, Roland

TITLE OF INVENTION: NOVEL AGOUTI-RELATED GENE

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: 1840 DEHAVILLAND DRIVE

CITY: THOUSAND OAKS

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/342,581

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/033,275

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: OLESKI, NANCY A

REGISTRATION NUMBER: 34,688

REFERENCE/DOCKET NUMBER: A-402A

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 54 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-342-581-8

Query Match 95.5%; Score 321; DB 4; Length 54;

Best Local Similarity 100.0%; Pred. No. 3.8e-27;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 57  
DB 1 REPRSSRCVRLHESCLGQVPCDPCATCYCRFNACFCYCRKLTANPCSR 54

## RESULT 10

US-09-031-902-2

Sequence 2, Application US/09031902

Patent No. 6228840

GENERAL INFORMATION:

APPLICANT: Wei, Edward T.

APPLICANT: Quillian, J. Mark

APPLICANT: Sadee, Wolfgang

APPLICANT: Vlasov, Guennady

APPLICANT: Chang, J.K.

TITLE OF INVENTION: MELANOCORTIN RECEPTOR ANTAGONISTS AND

MODULATORS OF MELANOCORTIN RECEPTOR ACTIVITY

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Majestic, Parsons, Siebert &amp; Hsue P.C.

STREET: Four Embarcadero Center, Suite 1100

CITY: San Francisco

STATE: California

COUNTRY: U.S.A.

ZIP: 94111-4106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/031,902

FILING DATE: 27-FEB-1998

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28,758

REFERENCE/DOCKET NUMBER: 2500.095050

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-248-5500

TELEFAX: 415-362-5418

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:



```

?      NAME: OLESKI, NANCY A
?      REGISTRATION NUMBER: 34,688
?      REFERENCE/DOCKET NUMBER: A-402A
?      INFORMATION FOR SEQ ID NO: 10:
?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 131 amino acids
?      TYPE: amino acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?      MOLECULE TYPE: protein
US-09-342-581-10

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Query Match	88.7%;	Score 298;	DB 4;	Length 131;
Best Local Similarity	91.1%;	Pred. NO. 2e-24;		
Matches 51; Conservative	1;	Mismatches 4;	Indels 0;	Gaps. 0;

```
0Y      2 QDREPRSSRRCVRLHESCLGQVPCCDDPCATCYCRFNAFCYCRKIGTAMNCSTRT 57  
       :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
76 QNRESHSRRCVRLHESCLGQVPCCDDPCATCYCRFNAFCYCRKIGTATMNCSTRT 131
```

```

RESULT 14
US-09-240-078-1
: Sequence 1, Application US/09240078
: Patent No. 6303749
: GENERAL INFORMATION:
: APPLICANT: Jaroslaski, Mark A.
: TITLE OF INVENTION: No. 6303749el Agouti and Agouti-Related Peptide Analogs
: FILE REFERENCE: A-569
: CURRENT APPLICATION NUMBER: US/09/240,078
: CURRENT FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 48
: TYPE: PRT
: ORGANISM: Human
US-09-240-078-1

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Query Match	85.1%	Score 286	DB 4	Length 48
Best Local Similarity	100.0%	Pred. No.	1.5e-23	
Matches 47; Conservative	0	Mismatches	0	Indels 0; Gaps 0;

QY 11 RCVRLHESCLGQQVPCCDPCAATCYCRFENAFICYCRKLTGMNPPCSRT 57  
|||||  
2 RCVRLHESCLGQQVPCCDPCAATCYCRFENAFICYCRKLTGMNPPCSRT 48

RESULT 15  
US-09-240-078-2

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: Sequence 2, Application US/09240078
: Patent No. 6303749
:
: GENERAL INFORMATION:
: APPLICANT: Jarosinski, Mark A.
: TITLE OF INVENTION: No. 6303749el Agouti and pigouti-Related Peptide Analogs
: FILE REFERENCE: A-569
: CURRENT APPLICATION NUMBER: US/09/240,078
: CURRENT FILING DATE: 1999-01-29
: NUMBER OF SEQ ID NOS: 55
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 2
:
: LENGTH: 32
: TYPE: PRT
:
: ORGANISM: Artificial Sequence
:

```

OTHER INFORMATION: Description of Artificial Sequence: AGRP Peptidase  
OTHER INFORMATION: Analog with synthetic amino acid (amino butyric  
OTHER INFORMATION: acid) at positions 12 and 15 and labeled as Xaa.  
US-09-240-078-2

Query Match	53.9%	Score 181;	DB 4;	Length 32;
Best Local Similarity	93.8%	Pred. NO. 8.4e-13;		
Matches 30; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

OY		16	HESCLGQVPCCDPCATCYCRFNFCYCRLK	477
D8		1	HESCLGQVPXCDDPKATCYCGRFNAFCYCRLK	329

Search completed: July 22, 2002, 17:18:53  
Job time: 333 sec

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